

92780

STIC-Biotech/ChemLib

From: Ibrahim, Medina A.
Sent: Tuesday, April 29, 2003 6:15 PM
To: STIC-Biotech/ChemLib
Subject: 10/010, 731

RECEIVED
APR 30 2003
STIC

Please run the following search:

1. A nucleotide sequence from position 18 to 507 of SEQ ID NO:10
2. A nucleotide sequence from position 105 to 242 of SEQ ID NO:13. Thanks

Medina A. Ibrahim
Patent Examiner
GAU:1638
CM1-9E03
mailbox:9E12
(703)306-5822

up 9203

Mary Jane Ruhl
Tech. Info. Specialist, STIC
TC-1600
CM-1, Room 6A-06
Phone: 605-1155

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 5/8/03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

THIS PAGE BLANK (USPTO)

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2003, 03:16:57 ; Search time 273.089 Seconds

(without alignments)

4040.728 Million cell updates/sec

Title: US-10-010-731-10_COPY_18_507

Perfect score

Sequence: 1 TGTCAAACACACACATAACA.....CAAAATAAAATAAAATAAA 490

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

```
Minimum DB seq length: 0
```

Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%

Maximum Match	100%
Maximum Match	100%

Listing first 45 summaries

1. N_Geneseq_101002.*
2. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
3. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
4. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
5. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
6. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
7. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
8. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
9. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
10. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
11. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
12. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
13. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
14. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
15. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
16. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
17. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
18. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
19. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
20. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
21. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
22. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
23. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
24. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	488	99.6	507	19	AAV39195	Antifungal polypep
2	486.4	99.3	430	19	AAV39186	Antifungal polypep
3	301.8	61.6	327	19	AAV39194	Antifungal polypep
4	234	47.8	250	19	AAV39187	Alfalfa plant anti
5	228.6	46.7	293	19	AAV39191	Antifungal polypep
6	208	42.4	468	21	AA249412	Pea defensin prot
7	179.8	36.7	200	19	AAV39190	Antifungal polypep
8	127.4	26.0	494	22	AAAD17530	Soybean Gly m2 pro
9	34	11.0	62	19	AAV39196	Antifungal polypep

C 10	49.4	10.1	16633	24	ABN79685	Human chemically m
C 11	48.6	9.9	9963	24	ABL32694	Human immune syste
C 12	46	9.4	6169	22	AAS46370	Tumour suppressor
C 13	46	9.4	6169	24	ABN80097	Human Chemically m
C 14	46	9.4	6557	24	ABL33001	Human immune syste
C 15	46	9.4	11922	21	AAAY0187	Plasmodium falciipa
C 16	45.8	9.3	6012	24	ABL34058	Human immune syste
C 17	45.4	9.3	83391	24	ABO67094	Human angiogenesis
C 18	45.2	9.2	5997	24	ABL33625	Human immune syste
C 19	45.2	9.2	6392	24	ABL33684	Human immune syste
C 20	45.2	9.2	6392	24	ABL34506	Human metastasis a
C 21	45	9.2	7025	24	ABK40060	Human chemically p
C 22	45	9.2	7025	24	AAS63351	Chemically pretreat
C 23	45	9.2	11029	22	AAS46414	Tumour suppressor
C 24	44.8	9.1	1216	24	ABL34361	Human immune syste
C 25	44.6	9.1	8172	24	ABL34573	Human metastasis a
C 26	44.6	9.1	8182	24	ABN80221	Human Chemically m
C 27	44.6	9.1	9155	24	ABL33463	Human immune syste
C 28	44.6	9.1	13584	24	ABL33615	Human immune syste
C 29	44.4	9.1	6533	24	ABL33709	Human immune syste
C 30	44.4	9.1	16217	24	ABL33624	Human immune syste
C 31	44.4	9.1	19653	24	ABL33335	Human immune syste
C 32	44.4	9.1	37973	24	ABL34196	Human immune syste
C 33	44.4	9.1	640681	24	ABA927187	Buchnera sp. genom
C 34	44.2	9.0	9515	22	AAS45453	Chemically pretrea
C 35	44.2	9.0	9515	24	ABN80245	Human chemically m
C 36	44.2	9.0	9515	24	ABK28308	DNA transcription
C 37	44	9.0	7110	22	AAS46490	Tumour suppressor
C 38	44	9.0	7110	24	ABL70588	Chemically treated
C 39	44	9.0	7110	24	ABL33557	Human immune syste
C 40	44	9.0	7110	24	AAS61291	Human gene regulati
C 41	44	9.0	34688	24	ABO67060	Human angiogenesis
C 42	43.6	8.9	7498	24	ABL33257	Human immune syste
C 43	43.6	8.9	18154	24	ABL33254	Human immune syste
C 44	43.4	8.9	6222	24	ABL32235	Human immune syste
C 45	43.4	8.9	6228	24	ABL70470	Chemically treated

ALIGNMENTS

RESULT 1
AAV39195
ID AAV39195 standard; DNA; 507 BP.

AC AAV39195;

DT 25-SEP-1998 (first entry)

DE Antifungal polypeptide AlfaFP1 mature sequence encoding DNA

KW Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
KW plant pathogenic fungus; AlfAFP1; AlfAFP2; ds.

Medicago sativa

key	Location/Qualifiers
EH . key	173..310
FT CDS	/*tag= a
FT	/product= "mature ALFALFP1"
FT	

PN W09826083-A1

PD 18-JUN-1998

PF 11-DEC-1997; 97WO-0522662.

PR 13-DEC-1996; 96US-0766355.

PA (MONS) MONSANTO CO.

PI Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS,

XX

This DNA encodes an antifungal polypeptide, AlAfP1 isolated from alfalfa plants (Medicago). The polypeptides AlAfP1 and AlAfP2 are useful to control plant fungi, especially pathogenic fungi, by transforming plant cells with a vector comprising sequences encoding AlAfP1 or AlAfP2 to allow expression of antifungally effective amounts of the polypeptide. Such transformed plants may be e.g. apple, wheat, cotton and especially potato. Micro-organisms may also be transformed to produce the polypeptides, and applied to plants to control plant fungi. The polypeptides can also be included with a suitable solvent in antifungal compositions and these can be administered to plants to control plant fungi. Such compositions and genetically engineered plants may also contain additional molecules e.g. the compositions can contain other antifungal agents or the plants contain DNA encoding insecticidal (e.g. *Bacillus thuringiensis*) proteins. The polypeptides are also useful to prepare antibodies useful to detect polypeptides or isolate other alfalfa plant antifungal protein antigens. The nucleic acids are useful to produce polypeptides and transgenic plants and as probes or primers in nucleic acid hybridisation e.g. to detect complementary sequences in samples, and to prepare mutants or isolate similar sequences from related species.

Query Match	99.6%	Score 488	DB 19	Length 507	
Best Local Similarity	100.0%	Pred. No.	2.6e-107		
Matches 490	Conservative 0	Mismatches 0	Indels 0	Gaps 0	

61 AATCTAATCAAACTATGGAGAAATAC TAGCTGGCTTATGCTTCCTTCTTGCTTC 12
 78 AATCTAATCAAACTATGGAGAAATAC TAGCTGGCTTATGCTTCCTTCTTGCTTC 13

0y 121 TCCTTTGTTGCACAGAAATTGTGGTGACAGAACCCAGAAATGTGAGAAATTTGGCAGATA 180
|||||
Db 138 TCCTTTGTTGCACAGAAATTGTGGTGACAGAACCCAGAAACATGTGAGAAATTTGGCAGATA 190

Qy 181 AATATAGGGGACCATGCTTTACTGGTGTGACACTCAGTCACACCAAGAGAACGCAG 2440
|||||
Db 198 AATATAGGGGACCATGCTTTACTGGTGTGACACTCAGTCACACCAAGAGAACGCAG 2575

0y 241 TTAGTGAAGGTGTAGGACGACTTCGCTGCTGTACTAAAGATGTTAAATGCATC 300
 |||||
 Db 258 TTACTGGAAGGTGTAGGACGACTTCGCTGCTGTACTAAAGATGTTAAATGCATC 317

QY 301 TCCGCCACATCAAGATGTGCATGGATAGTCTTTATATAAATCTTAATAATAAATG 366
|||
Db 318 TCCGCCACATCAAGATGTGCATGGATAGTCTTTATATAAATCTTAATAATAAATG 372
|||

361 CACGAGTATAGCTACAACTTCATCTATATATATAGACTCATATATCGNCATPAACGATATTA 420
 378 CACGAGTATAGCTACAACTTCATCTATATATATAGACTCATATATCGNCATPAACGATATTA 437
 420

421 GTTATGCACTTCTATCATATGGAATAAACATCAATAGTAAATTTCGNTCCAAAAAAA 480
438 GTTATGCACTTCTATCATATGGAATAAACATCAATAGTAAATTTCGNTCCAAAAAAA 480
db

```

0y      481 AAAAAAAAAA 490
         | | | | | | | |
0b      408 AAAAAAAAAA 507

```

AC	AAV39186;
XX	
DT	01-OCT-1998 (first entry)
XX	

KW Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
KW plant pathogenic fungus; AlfaFP1; AlfaFP2; ss.

aa
OS
Medicago sativa.

FH	Key	Location/Qualifiers
FM	CDS	75 203

```

FT      /tag= a
FT      /trans] except= (pos:129..131, aa:Glu)

```

FT	/product-
FT	75.155
FT	slq_peptide

mat_peptide

PN WO9826083-A1.

18-JUN-1998

PF 11-DEC-1997; 97WO-US22662.
XX

PR 13-DEC-1996; 96US-0766355.
XX

PA (MONS) MONSANTO CO. .
XX

FD MAKING S, LIVING O,
XX

DR P-PSDB; AAW61967.

PT - Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s), used to control plant pathogenic fungi and to produce transformed

PT plants with increased fungal resistance

PS Claim 5; Fig 1; 9/pp; English.
XX

CC alfalfa plants (Medicago). The polypeptides ALFAFP1 and ALFAFP2 are

transforming plant cells with a vector comprising sequences encoding

of the polypeptide. Such transformed plants may be e.g. apple, wheat
cc cotton and especially potato. Micro-organisms may also be transformed

to produce the polypeptides, and applied to plants to control plant growth. The polypeptides can also be included with a suitable solvent

cc antifungal compositions and these can be administered to plants to
cc control plant fungi. Such compositions and genetically engineered pl

cc other antifungal agents or the plants contain DNA encoding insecticidal
cc may also contain additional molecules e.g. the compositions can contain
cc.

(e.g., bacillus anthracis) proteins. The polypeptides are also used to prepare antibodies useful to detect polypeptides or isolate other

to produce polypeptides and as probes or primers for the detection of the corresponding genes in transgenic plants and as probes or primers for the detection of the corresponding genes in transgenic plants and as probes or primers for the detection of the corresponding genes in transgenic plants.

CC samples, and to prepare mutants or isolate similar sequences from related CC species

Sequence 490 BP: 182 A: 85 C: 85 G: 136 T: 2 other
XX
50

Query Match	99.3%	Score 486.4	DB 19	Length 490
Best Local Similarity	99.8%	Pred. No. 6.2e-107		
Matches 489; Conservative	0	Mismatches 1	Indels 0	Gaps 0


```

OY 1 TGTCAACACACATACATACATAGTACCGTGCATTTAAATTTATATATTCATC 60
DB 1 TGTCAACACACATACATACATAGTACCGTGCATTTAAATTTATATATTCATC 60
OY 61 AATCTAATCAAACTATGAGAGAAATATCAAGTGGCTTATGCTTCTTCTGTTTC 120
DB 61 AATCTAATCAAACTATGAGAGAAATATCAAGTGGCTTATGCTTCTTCTGTTTC 120
OY 121 TCTTTGTGACAGAAATTTGTGTGACAGAAACCAATCATGTGAAATTTGGCAGATA 180
DB 121 TCTTTGTGACAGAAATTTGTGTGACAGAAACCAATCATGTGAAATTTGGCAGATA 180
OY 181 AATATAGGGGACCATGCTTTAGTGGTGTGACACTCAGTGCACCAACCAAGAGAGAGAG 240
DB 181 AATATAGGGGACCATGCTTTAGTGGTGTGACACTCAGTGCACCAACCAAGAGAGAGAG 240
OY 241 TTAAGTGAAGGTGTAGAGGAGCACTCCGCTGCTGCTGCTACTAAAAGATGTTAAATGATC 300
DB 241 TTAAGTGAAGGTGTAGAGGAGCACTCCGCTGCTGCTGCTACTAAAAGATGTTAAATGATC 300
OY 301 TCCCTCAACATCAGATGTGCATGATGATGCTTTATATATAAATTAATTAATGATG 360
DB 301 TCCCTCAACATCAGATGTGCATGATGATGCTTTATATATAAATTAATTAATGATG 360
OY 361 CACGAGATATAGCTACACTTCTATATATATATGACTCAATATGCGCATTAAGCTATTA 420
DB 361 CACGAGATATAGCTACACTTCTATATATATATGACTCAATATGCGCATTAAGCTATTA 420
OY 421 GTTATGCACTTCTATCATATATGGAATTAACATCAATTAATGTTGTTCCAAAAAATA 480
DB 421 GTTATGCACTTCTATCATATATGGAATTAACATCAATTAATGTTGTTCCAAAAAATA 480
OY 481 AAAAAAAAAA 490
DB 481 AAAAAAAAAA 490

RESULT 3
AAV39187
ID AAV39187 standard; DNA; 327 BP.
XX
AC AAV39187;
XX
DT 25-SEP-1998 (first entry)
XX
DE Antifungal polypeptide AlfaFP2 3' region.
XX
KW Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
KM plant pathogenic fungus; AlfaFP1; AlfaFP2; ds.
XX
OS Medicago sativa.
XX
FN W09826083-A1.
XX
PD 18-JUN-1998.
XX
PE 11-DEC-1997; 97WO-US22662.
XX
PR 13-DEC-1996; 96US-0766355.
XX
PA (MONS ) MONSANTO CO.
XX
PI Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS.
XX
DR WPI: 1998-348537/30.
XX
PT Antifungal polypeptide(s) and genes isolated from alfalfa plant(s)
PT used to control fungal pathogenic fungi and to produce transformed
PT plants with increased fungal resistance
XX
PS Claim 18; Page 77; 97pp; English.
XX
CC This sequence represents the 3' region of the DNA encoding an antifungal

```

```

CC polypeptide, AlfaFP2 isolated from alfalfa plants (Medicago). The
CC polypeptides AlfaFP1 and AlfaFP2 are useful to control plant fungi.
CC especially pathogenic fungi, by transforming plant cells with a vector
CC comprising sequences encoding AlfaFP1 or AlfaFP2 to allow expression of
CC antifungally effective amounts of the polypeptide. Such transformed
CC plants may be e.g. apple, wheat, cotton and especially potato.
CC Micro-organisms may also be transformed to produce the polypeptides, and
CC applied to plants to control plant fungi. The polypeptides can also be
CC included with a suitable solvent in antifungal compositions and these can
CC be administered to plants to control plant fungi. Such compositions and
CC genetically engineered plants may also contain additional molecules e.g.
CC the compositions can contain other antifungal agents or the plants
CC contain DNA encoding insecticidal (e.g. Bacillus thuringiensis)
CC proteins. The polypeptides are also useful to prepare antibodies useful
CC to detect polypeptides or isolate other alfalfa plant antifungal protein
CC antigens. The nucleic acids are useful to produce polypeptides and
CC transgenic plants and as probes or primers in nucleic acid hybridisation
CC e.g. to detect complementary sequences in samples, and to prepare mutants
CC or isolate similar sequences from related species.
XX
SQ Sequence 327 BP; 125 A; 49 C; 60 G; 91 T; 2 other:
Query Match 61.6%; Score 301.8; DB 19; Length 327;
Best Local Similarity 97.6%; Pred. No. 7.2e-63;
Matches 319; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
OY 165 GAGAAATTTGGCAGATTAATATAGGGAGACCAGTCTTATGTTGGACATCAGTCACA 224
DB 1 GAGAAATTTGGCAGATTAATATAGGGAGACCAGTCTTATGTTGGACATCAGTCACA 60
OY 225 ACCAAGAGAAACGAGTAGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 284
DB 61 ACCAAGAGAAACGAGTAGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
OY 285 AGATGTTAAATGATCTCTCCACATCAAGATGTCATGATGATGATGATGATGATGATGATG 344
DB 121 AGATGTTAAATGATCTCTCCACATCAAGATGTCATGATGATGATGATGATGATGATGATG 180
OY 345 CTAAATTAATTAATTAATGACGACGATAGCTACAACTTCTATATATATATGACATCAATA 403
DB 181 CTAAATTAATTAATTAATGACGACGATAGCTACAACTTCTATATATATATATATATATAT 240
OY 404 TCGNCATATAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 463
DB 241 TCGNCATATAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
OY 464 TCGTNTCCAAAAA 490
DB 301 TCGTNTCCAAAAA 327

RESULT 4
AAV39187
ID AAV39187 standard; DNA; 250 BP.
XX
AC AAV39187;
XX
DT 25-SEP-1998 (first entry)
XX
DE Alfalfa plant antifungal polypeptide AlfaFP1 encoding DNA.
XX
KW Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
KM plant pathogenic fungus; AlfaFP1; AlfaFP2; ds.
XX
OS Medicago sativa.
XX
OS
XX
FH Key Location/Qualifiers
FH CDS 105..242
FH /tag= a
FH /product= "mature AlfaFP1"
XX
XX W09826083-A1.
XX

```

PD 18-JUN-1998.
XX
XX 11-DEC-1997; 97WO-US22662.
XX
PR 13-DEC-1996; 96US-0766355.
XX
XX (MONS) MONSANTO CO.
XX
PI Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;
XX WPI: 1998-348537/30.
DR P-PSDB; AAM61964.
PT Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
PT - used to control plant pathogenic fungi and to produce transformed
PT plants with increased fungal resistance
XX
PS Claim 3; Page 78; 97pp; English.
XX
XX This DNA encodes an antifungal polypeptide, AlfAP1 isolated from
CC alfalfa plants (Medicago). The polypeptides AlfAP1 and AlfAP2 are
CC useful to control plant fungi, especially pathogenic fungi, by
CC transforming plant cells with a vector comprising sequences encoding
CC of the polypeptide. Such transformed plants may be e.g. apple, wheat,
CC cotton and especially potato. Micro-organisms may also be transformed
CC to produce the polypeptides, and applied to plants to control plant
CC fungi. The polypeptides can also be included with a suitable solvent in
CC antifungal compositions and these can be administered to plants to
CC control plant fungi. Such compositions and genetically engineered plants
CC may also contain additional molecules e.g. the compositions can contain
CC other antifungal agents or the plants contain DNA encoding insecticidal
CC (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful
CC to prepare antibodies useful to detect polypeptides or isolate other
CC alfalfa plant antifungal protein antigens. The nucleic acids are useful
CC to produce polypeptides and transgenic plants and as probes or primers in
CC nucleic acid hybridisation e.g. to detect complementary sequences in
CC samples, and to prepare mutants or isolate similar sequences from related
CC species.
XX
SQ Sequence 250 BP; 73 A; 48 C; 64 G; 65 T; 0 other;
Query Match 47.8%; Score 234; DB 19; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
YY 60 CAATCTATCAAACTATGAGAGAGAAATCACTAGCTTATGCTTCTTCTTGGT 119
DB 9 CAATCTATCAAACTATGAGAGAGAAATCACTAGCTTATGCTTCTTCTTGGT 68
YY 120 CTCTTGTGACAGAAATTTGTTGTGACAGAGCCAGAACATGTGAGAAATTTGGCAGAT 179
DB 69 CTCTTGTGACAGAAATTTGTTGTGACAGAGCCAGAACATGTGAGAAATTTGGCAGAT 128
YY 180 AAAATATGGGAGACATGCTTGTAGTGTTGTGACACCTACCTGACACCAACCAAGAGAGCA 239
DB 129 AAAATATGGGAGACATGCTTGTAGTGTTGTGACACCTACCTGACACCAACCAAGAGAGCA 188
YY 240 GTTAGTGAAGGTAGGAGAGACTCCGCTGCTGCTGCTAAAGATTTAA 293
DB 189 GTTAGTGAAGGTAGGAGAGACTCCGCTGCTGCTGCTAAAGATTTAA 242
RESULT 5
ID AAV39191
XX AAV39191 standard; DNA: 293 BP.
AC AAV39191;
XX
XX 25-SEP-1998 (first entry)
XX
DE Antifungal polypeptide AlfAP2 coding sequence.
XX

KW Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
XX plant pathogenic fungus; AlfAP1; AlfAP2; ds.
XX
OS Medicago sativa.
XX
XX
XX W09826083-A1.
XX
PD 18-JUN-1998.
XX
XX 11-DEC-1997; 97WO-US22662.
XX
XX 13-DEC-1996; 96US-0766355.
XX
XX (MONS) MONSANTO CO.
XX
PI Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;
XX WPI: 1998-348537/30.
DR
XX
XX Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
PT - used to control plant pathogenic fungi and to produce transformed
PT plants with increased fungal resistance
XX
PS Claim 18; Page 75; 97pp; English.
XX
XX This represents a coding sequence of an antifungal polypeptide, AlfAP2
CC isolated from alfalfa plants (Medicago). The polypeptides AlfAP1 and
CC AlfAP2 are useful to control plant fungi, especially pathogenic fungi,
CC by transforming plant cells with a vector comprising sequences encoding
CC AlfAP1 or AlfAP2 to allow expression of antifungally effective amounts
CC of the polypeptide. Such transformed plants may be e.g. apple, wheat,
CC cotton and especially potato. Micro-organisms may also be transformed
CC to produce the polypeptides, and applied to plants to control plant
CC fungi. The polypeptides can also be included with a suitable solvent in
CC antifungal compositions and these can be administered to plants to
CC control plant fungi. Such compositions and genetically engineered plants
CC may also contain additional molecules e.g. the compositions can contain
CC other antifungal agents or the plants contain DNA encoding insecticidal
CC (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful
CC to prepare antibodies useful to detect polypeptides or isolate other
CC alfalfa plant antifungal protein antigens. The nucleic acids are useful
CC to produce polypeptides and transgenic plants and as probes or primers in
CC nucleic acid hybridisation e.g. to detect complementary sequences in
CC samples, and to prepare mutants or isolate similar sequences from related
CC species.
XX
SQ Sequence 293 BP; 82 A; 60 C; 72 G; 77 T; 2 other;
Query Match 46.7%; Score 228.6; DB 19; Length 293;
Best Local Similarity 89.1%; Pred. No. 2.2e-45;
Matches 246; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
YY 1 TGTAAACACACACATACATAGTACCGGAGCATTAATTAATTAATTAATTCATC 60
DB 18 TGTAAACACACACATACATAGTACCGGAGCATTAATTAATTAATTAATTCATC 77
YY 61 AATCTATCAAACTATGAGAGAGAAATCACTAGCTTATGCTTCTTCTTGGTTC 120
DB 78 AATCTATCAAACTATGAGAGAGAAATCACTAGCTTATGCTTCTTCTTGGTTC 137
YY 121 TCTTTGTGACAGAAATTTGTTGTGACAGAGCCAGAACATGTGAGAAATTTGGCAGATA 180
DB 138 TCTTTGTGACAGAAATTTGTTGTGACAGAGCCAGAACATGTGAGAAATTTGGCAGATA 197
YY 181 AATATAGGGGACATGCTTGTAGTGTTGTGACACCTACCTGACACCAACCAAGAGAGCAG 240
DB 198 CATACAGGGGACATGCTTGTAGTGTTGTGACACCTACCTGACACCAACCAAGAGAGCAG 257
YY 241 TTAGTGAAGGTAGGAGAGACTCCGCTGCTGCT 276
DB 258 TTAGCGGAGGTAGGAGAGACTCCGCTGCTGCT 293

[illegible]

XX	01-SEP-2000; 2000DE-1043826.
PR	(EPIC-) EPIGENOMICS AG.
PA	Olek A., Piepenbrock C., Berlin K;
XX	WP1: 2002-139908/17.
DR	
XX	
PT	Novel nucleic acid useful for diagnosis and therapy of diseases
PT	associated with development genes such as diabetes; comprises a
PT	sequence of a segment of chemically pretreated DNA of genes associated
PS	with development -
XX	
XX	Claim 1; SEQ ID NO 2; 27pp; English.
CC	
CC	The invention relates to a nucleic acid (I) comprising a sequence at
CC	least 18 bases in length of a segment of chemically pretreated DNA (II)
CC	of genes associated with development selected from 87 genes listed in
CC	the specification such as ACCCN, ADEN, or APD1 and comprising one of 350
CC	sequences (AAN7984-ABN8033) or their complements. The invention is
CC	useful for the diagnosis or therapy of diseases associated with
CC	development genes, in particular disease related to homeobox containing
CC	genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes
CC	associated with congenital heart disease, epilepsy, diseases related to
CC	histone deacetylation, Curarino syndrome, diseases related with the
CC	development of the brain and limb girdle muscular dystrophy and dwarfism.
CC	Oligomers specific to each of the genes are useful for detecting the
CC	methylation state of all CpG dinucleotides within the 350 sequences or
CC	(II) and their complementary sequences, as primer oligonucleotides for
CC	the amplification of the 350 sequences, (II) and/or their complements and
CC	as oligomer probes for detecting the cytosine methylation state and/or
CC	single nucleotide polymorphisms (SNPs).
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification but is based on sequence information supplied to Derwent by
CC	the European Patent Office.
XX	
SQ	Sequence 16633 BP; 5259 A; 142 C; 3255 G; 7977 T; 0 other:
	Query Match 10.1%; Score 49.4; DB 24; Length 16633;
	Best Local Similarity 52.2%; Pred. No. 0.032;
	Matches 107; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
QY	284 AAGATGTAAATGGATCTCCTCCAACATCAATGTCATGGAATTGTTTATAATAA 343
Db	14559 AAAACTTAATTATATCTCTTTTCAACTTTAAATGCCACTTTTAAATCTTAAATAATTA 14500
QY	344 ACTAAATTAATTAATGACGCAGATAGTGCTCACTCATCATATATATGACGTCAATA 403
Db	14499 AAACCACAATTAACAAAAAAAATTAACCAAACATTAATTAACATATATATACATT 14440
QY	404 TCGNGCATACAGTATAGTATGACACTTCTATCATATGAGAATAACATCAATAAAGTAATT 463
Db	14439 TCATATATTTTACCTACTACTATAATATATTAATAATTCTTAAACAAAAAACCTTAAT 14380
QY	464 TCGTNTCCAAAAAAAATAAAAA 488
Db	14379 TCTATTACCACCAAAAAAACAANA 14355
RESULT 11	
ABLJ32694/c	
ID	ABLJ32694 standard; DNA; 9963 BP.
AC	
XX	ABLJ32694;
XX	
DT	26-MAR-2002 (first entry)
XX	
DE	Human immune system associated gene SEQ ID NO: 667.
XX	
KW	Human: immune system disease; cytosine methylation; antislammatic;
KW	antileukosclerotic; antihaemic; cytostatic; nootropic;
KW	neuroprotective; anti-HIV; anticouvalant; ophthalmological;
KW	antirheumatic; antirthritis; antididiabetic; antipsoriasis;

KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
 KW gene; ds.
 OS Homo sapiens.
 XX WO200200928-A2.
 XX PD 03-JAN-2002.
 XX PF 02-JUL-2001; 2001WO-EP07537.
 XX PR 30-JUN-2000; 2000DE-1032529.
 XX PR 01-SEP-2000; 2000DE-1043826.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI: 2002-130909/17.
 XX PT Nucleic acid comprising fragment of chemically modified gene, useful
 PT for diagnosis and treatment of diseases associated with abnormal
 PT cytosine methylation
 XX PS Claim 1; SEQ ID NO 667; 32pp + Sequence Listing; German.
 CC The present invention provides a number of human immune system associated
 CC genes which are modified by the methylation of cytosines. The sequences
 CC can be used in the diagnosis and treatment of immune system disorders,
 CC including eye diseases such as retinopathy, neovascular glaucoma and
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
 CC diseases. The present sequence is a gene of the invention.
 SO Sequence 9963 BP; 2520 A; 180 C; 2578 G; 4685 T; 0 other;
 Query Match 9.9%; Score 48.6; DB 24; Length 9963;
 Best Local Similarity 51.7%; Pred. No. 0.045;
 Matches 108; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
 OY 282 AAAAGATGTTAAATGAGTCTCTCCACATCAAGATGTCATGATGCTTTATATA 341
 DB 3726 ACAATTAATCTTAACCTTCTCTACCTCACTCTCTCTATATATATATATA 3667
 OY 342 AAATTAATTAATTAATGACGAGTATAGTCAACTGATCATCATATATATATAT 401
 DB 3666 ATTCTCTACTCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3607
 OY 402 TATGNGCATTAAGTATGATGCACTTCTATCATATGAAATTAACATCAATTA 461
 DB 3606 AATTAATACCTTAACATTAATTAATTAATTAATTAATTAATTAATTAAT 3547
 OY 462 TTTCGTTCCAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 490
 DB 3546 AAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3518
 RESULT 12
 ID AAS46370/c
 AAS46370 standard; DNA; 6169 BP.
 XX AAS46370;
 XX AC
 XX 18-DEC-2001 (first entry)
 XX DT
 DE Tumour suppressor gene derived chemically modified sequence #92.
 KW Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
 KW cancer; tumour; CPG dinucleotide; single-nucleotide polymorphism; SNP;
 KW cytosine methylation; ds.

XX OS Homo sapiens.
 XX PN WO200168912-A2.
 XX PD 20-SEP-2001.
 XX PF 15-MAR-2001; 2001WO-EP02955.
 XX PR 15-MAR-2000; 2000DE-1013847.
 XX PR 06-APR-2000; 2000DE-1019058.
 XX PR 07-APR-2000; 2000DE-1019173.
 XX PR 30-JUN-2000; 2000DE-1032529.
 XX PR 01-SEP-2000; 2000DE-1043826.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI: 2001-602752/68.
 XX PT Fragments of chemically modified genes associated with tumour suppressor
 PT genes and oncogenes, useful in designing primers and probes for
 PT analysing diseases associated with cytosine methylation state e.g.
 PT cancer
 XX PS Claim 1; SEQ ID NO 92; 27pp; English.
 CC The invention relates to a nucleic acid comprising a sequence of 18
 CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
 CC bisulphite, of genes associated with tumour suppression and
 CC oncogenes having a sequence taken from 536 (actually 533 since
 CC numbers 408, 438 and 500 are missing from the sequence listing) sequences
 CC (Ss) and sequences complementary to (Ss). The nucleic acid may be a
 CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may
 CC form part of a set of probes for detecting the cytosine methylation state
 CC and/or single nucleotide polymorphisms and also to be used in an
 CC array for analysing diseases associated with CPG dinucleotides e.g.
 CC cancers and tumours. The probes can also be used in a method for
 CC ascertaining genetic and/or epigenetic parameters for the diagnosis
 CC and/or therapy of existing diseases or the predisposition to specific
 CC diseases, by analysing cytosine methylations. The parameters may be
 CC compared to another set of genetic and/or epigenetic parameters, the
 CC differences serving as basis for diagnosis and/or prognosis events which
 CC are disadvantageous to patients. The present sequence is one of the
 CC 533 genomic sequences derived from tumour suppressor genes and
 CC oncogenes. Sequences with even numbered Seq ID numbers are the
 CC complementary sequence of the corresponding odd numbered sequence (e.g.
 CC ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence
 CC is missing).
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 SO Sequence 6169 BP; 1840 A; 112 C; 1192 G; 3025 T; 0 other;
 Query Match 9.4%; Score 46; DB 22; Length 6169;
 Best Local Similarity 56.9%; Pred. No. 0.17;
 Matches 82; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
 OY 347 AAATTAATTAATTAATGACGAGTATAGTCAACTCTATATATATGACTCAATTCG 406
 DB 2534 AAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 466
 OY 407 NGCATAAGTATAGTATGACCTTCTATCATATGGAATTAACATCAATTAATTCG 466
 DB 2474 TACAAAACATATCTTAAATTAATTAATTAATTAATTAATTAATTAATTA 2415
 OY 467 TTTCCAAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 490
 DB 2414 AAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2391

QY 418 TTAGTATGCACTTCATCATATGCAATTAACATCAATAGTAATTCCTNCCAAAAA 477
DB 4317 TTAATAAACTCATCAACACTTTCATCCCACTCTCAATCAATTAACAAAAA 4258
QY 478 AAAAAAAAAA 489
DB 4257 AAAAAAATAAAAA 4246

RESULT 15

AAA70187
ID AAA70187 standard; DNA; 11922 BP.

AC AAA70187;

DT 07-NOV-2000, (first entry)

DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:320.

KW Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine;
antimalarial; malaria; protozoacide; infection; insecticide; ds.

OS Plasmodium falciparum.

PN WO200025728-A2.

PD 11-MAY-2000.

PF 05-NOV-1999; 99WO-US26796.

PR 05-NOV-1998; 98US-0107131.

PA (HOFF/) HOFFMAN S.
PA (CARU/) CARUCCI D.
PA (GARD/) GARDNER M.
PA (VENT/) VENTER J C.

PI Hoffman S, Carucci D, Gardner M, Venter JC;

DR WPI; 2000-365347/31.

PT Proteins encoded by chromosome 2 of the human malarial parasite,
Plasmodium falciparum, useful as antimalarial vaccines and in the
diagnosis of P.falciparum infection -

PS Disclosure: Page 516-519; 577pp; English.

CC The present invention describes proteins and their fragments (I) encoded
CC by chromosome 2 of the human malarial parasite, Plasmodium falciparum.
CC Also described are: (1) nucleotide sequences (II) encoding (I); and (2)
CC vaccines against P. falciparum infection comprising (I) or (II).
CC (I) and (II) are useful for the development of vaccines against
CC P. falciparum infection. (I) and polyclonal antisera or a monoclonal
CC antibody raised to immunogens comprising the sequences of (I), are
CC useful in the detection of infection with P. falciparum. Furthermore,
CC (I) (especially when they are rifins or secreted or membrane proteins)
CC can aid the identification of drugs to treat or prevent P. falciparum
CC infection, or they can be used to identify drug resistance in
CC P. falciparum. Sequencing of the Plasmodium chromosome 2 and the
CC subsequent identification of proteins encoded by it will help to expand
CC our understanding of parasite biology, a process hampered by the
CC complexity of the parasitic lifecycle, and provide new targets for
CC vaccine and drug development. Parasite resistance to drugs and mosquito
CC resistance to insecticides have led to a resurgence of malaria in many
CC parts of the world, and there is a pressing need for vaccines and new
CC drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide
CC and protein sequences given in the present invention, but which are not
CC specifically mentioned within the specification.

SO Sequence 11922 BP; 5402 A; 948 C; 1343 G; 4229 T; 0 other;

Query Match 9.4%; Score 46; DB 21; Length 11922;
Best Local Similarity 55.0%; Pred. No. 0.19;

Matches 88; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
QY 331 TCTTATATATAAACTTAATAATAATGACGAGATATAGCTACCACTTCATCTATAT 390
DB 8019 TTTACATTAATTTTAAATAATGAAATTAATGATGAAATATATTAACCTTACCAAAAGTTT 8078
QY 391 AATGACTCAATATGCGCATPACGTATATGATGCACTTCATCATATGGAATTAACA 450
DB 8079 AATGATGTAATAATACAGATTATGTGTTATGTTTAAATTAATTAATTAATTAACA 8138
QY 451 TCAATAGTAATTTGTCATCCAAAAAATAAAAAA 490
DB 8139 TAAAGAAATTTATCAGAAATGAATAATTAATTAATAAGAGAA 8178

Search completed: May 8, 2003, 05:53:59
Job time : 287.089 secs

FEATURES	source
CDs	1. 406 /organism="Medicago sativa" /db_xref="taxon:3879" 75. .293 /note="alfAFP; defensin" /codon_start=1 /product="antifungal protein precursor" /protein_id="AAG0321.1" /db_xref="GI:11762086" /translation="MEKSLAGLFLVLEVAOEIVTEARICENTLADYKGFPSGS CDFTTKENAVNSGRCDPFRMCYTKRC" 75. .155 156. .290 mat_peptide slg_peptide /product="antifungal protein" 140 a 74 c 78 g 114 t
BASE COUNT	140 a 74 c 78 g 114 t
ORIGIN	
Query Match	82.9%; Score 406; DB 8; Length 406;
Best Local Similarity	100.0%; Prod. No. 2.1e-74; Indels 0; Gaps 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 TGTCAACACACACATTAACATTAAGTACCGGTGAGTCATTAATTAATTAATTCATC 60	
Db 1 TGTCAACACACACATTAACATTAAGTACCGGTGAGTCATTAATTAATTAATTCATC 60	
QY 61 AATCTAATCAACTATGTGAGAGAAGAAATACATGCTGAGTTCCTCTCTTGCTGCTC 120	
Db 61 AATCTAATCAACTATGTGAGAGAAGAAATACATGCTGAGTTCCTCTCTTGCTGCTC 120	
QY 121 TCTTTGTGCAAGAATTTGGTGGAGAGAACGACAAACATGTGAGAAATTTGGCAGATA 180	
Db 121 TCTTTGTGCAAGAATTTGGTGGAGAGAACGACAAACATGTGAGAAATTTGGCAGATA 180	
QY 181 AATATAGGGGACCATGCTTTTAGTGGTGTGACACTCATGTGCACAACAAAGAGACGAG 240	
Db 181 AATATAGGGGACCATGCTTTTAGTGGTGTGACACTCATGTGCACAACAAAGAGACGAG 240	
QY 241 TTATGAGGAAGTGTATGGGACGACTCCGCTGCTGGTGTACTTAAAGATGTTAAATGATC 300	
Db 241 TTATGAGGAAGTGTATGGGACGACTCCGCTGCTGGTGTACTTAAAGATGTTAAATGATC 300	
QY 301 TCTCTCAACATCAAGATGTGCATGGAATAGCTTTATATATAAACTAATTAATTAATG 360	
Db 301 TCTCTCAACATCAAGATGTGCATGGAATAGCTTTATATATAAACTAATTAATTAATG 360	
QY 361 CACGAGATATAGCTCAACATTCATCTATATATATATGACTCAATATG 406	
Db 361 CACGAGATATAGCTCAACATTCATCTATATATATGACTCAATATG 406	
RESULT 2	
PEADRR230A	468 bp mRNA linear PLN 11-FEB-2002
LOCUS	Pea (p1230) disease resistance response protein 230 (DRR230-a)
DEFINITION	mRNA, complete cds.

ACCESSION	L01578	S86895
VERSION	L01578.1	GI:169073
KEYWORDS	cysteine-rich protein; disease resistance response protein 230; pathogenesis-related protein.	
SOURCE	Pisum sativum.	
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.	
REFERENCE	1 (bases 1 to 468)	
AUTHORS	Chiang,C.C. and Hadwiger,L.A.	
TITLE	The Fusarium solani-induced expression of a pea gene family encoding high cysteine content proteins	
JOURNAL	Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)	
MEDLINE	92190628	
PUBMED	1799696	
COMMENT	On Feb 8, 2002 this sequence version replaced gi:247416.	
FEATURES	Location/Qualifiers	
source	1..468	/organism="Pisum sativum"
		/strain="Alaska"
		/db_xref="taxon:3888"
		/tissue_type="pod tissue treated with Fusarium solani conidia"
		/dev_stage="Immature"
gene	1..468	/gene="DRR230-a"
CDS	78..296	/gene="DRR230-a"
		/function="unknown"
		/standard_name="pathogenesis related protein"
		/note="p1230"
		/codon_start=1
		/evidence=experimental
		/product="disease resistance response protein"
		/protein_id="AA7917.1"
		/db_xref="GI:169074"
		/translation="MERKSLACLSEFLLLVFEVAOEIVSEANTCENLAGSYKVCGEGGCDRHRTQEGALISGRCHDFRCMCTKNC"
		159..293
mat_peptide		/gene="DRR230-a"
		/product="disease resistance response protein"
		/function="unknown"
		/note="determined by in vitro cleavage with microsomal membranes"
		/evidence=experimental
BASE COUNT	153 a	88 c 84 g 143 t
ORIGIN		
Query Match	42.4%	Score 208; DB 8; Length 468;
Best Local Similarity	72.2%;	Pred. No. 2.3e-33;
Matches 345; Conservative	0; Mismatches 112; Indels 21; Gaps 5;	
Dy	4 CAAACACACATAATAGTACCCTGGTCATTAAATTTATATATTCATCAAT	63
Dy	6 CACAACACACATATACATTAAGTAGAGTAGTCATATTTAAGTTTTATATCATCACT	65
OY	64 -CTAATCAACTANTGAGAGAATCACTAGCTGGCTTATGCTCTCTTGTTGTTCTC	122
Dy	66 ACTTAAGGAAGCCATGGAAGAAACACTAGTCTGTCTCTCTCTCTCTCTCTCTC	125
OY	123 TTTGTTGCACAAGAAATGTGGTGCACAAGGCCAAGCAATGAGAAATTTGGCAGATAAA	182
Dy	126 TTTGTTGCACAAGAAATGTGGTGCAGTACCGCTACTGTAGAACACAGAGGCCCAAT	245
OY	183 TATAGGGACCATGCTTATAGTGTGTGACACTCACTGACACACCAAGAGAGAGCAGTT	242
Dy	186 TATAGGGAGATATGCTTGGTGAGTGTACCGCTACTGTAGAACACAGAGGCCCAAT	245
OY	243 AGTGAAGGTAGGAGACACTCCGCTGCTGCTGTACTAAAGATGTTAAATGATCTC	302
Dy	246 AGCGCACATCAGGAGATCTTCGCTGGTGTGCTACATAAAACCTGTTAAATCCCTTT	305

D	b	126	TTTGTGCACAAAGAAATAGTGCTGAGTCAGCAACAACATGTGGAAATTGTGCTGTCCA	185
Q	y	183	TATAGGGACCAGCCTTAGTGGTTGTGACACTACTCTCACACCAAGAAGAGCGCAGTT	242
D	b	186	TATAAGGAGATATGCTTGGTGGATGTACCGCTACTAGAACACAGAGGCCAATY	245
Q	y	243	AGTGAAGCTAGGAGACGATCCGCGCGTCTACTAAAGATGTAAATGATCTC	302
D	b	246	AGCGCAATCATCAGGAGACTTTCGCTGGTGTCACATAAAAACGTGTAATTCCTTTY	305
Q	y	303	CTCCACATCATAGATGTGTCATGATAGTCTTTTATATAAAAACTAAATAAATAATGCA	362
D	b	306	CTCCACACCCAAACACACCCATATATAT -ACTATAATATATATATATATATATAT	357
Q	y	363	CGCAGTATAGCTACAACTTCACTATATATATATAGCTCAATATCGNCATTAACGTATAGT	422
D	b	358	-AGTGTGTTTCCAAATCTTATGTGTGT -ACTCAATATCGGTATTAACGTGTGTT	410
Q	y	423	TATGACACT-----CTATCATATGGAATAAATCAATCAATAGAAATTCGTNCCAAA	475
D	b	411	TATGACTTTTATCATATCATATGGAATAAATAAGTAATCAATCATTCCTTCCAAA	468
R	E	S		
RESULT		4		
LOCUS		AF139018	363 bp mRNA linear PLN 02-JAN-2001	
DEFINITION		Pisum sativum disease resistance response protein 230 precursor		
ACCESSION		(DNR230) mRNA, complete cds.		
VERSION		AF139018		
KEYWORDS		AF139018.1 GI:12002298		
SOURCE				
ORGANISM		Pisum sativum.		
		Pisum sativum.		
		Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
		Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;		
		Pisum.		
REFERENCE		1 (bases 1 to 363)		
AUTHORS		Sevenstrand,H., Brosche,M. and Strid,A.		
TITLE		Stress-induced disease resistance response protein 230 cDNA from		
JOURNAL		Pisum sativum cv. Greenfeast		
REFERENCE		Unpublished		
AUTHORS		2 (bases 1 to 363)		
TITLE		Sevenstrand,H., Brosche,M. and Strid,A.		
JOURNAL		Direct Submission		
		Submitted (29-MAR-1999) Biochemistry and Biophysics, Goteborg		
		University, Medicinaregatan 9c, P.O. Box 462, Goteborg S-40530,		
		Sweden		
FEATURES				
SOURCE		Location/Qualifiers		
		1..363		
		/organism="Pisum sativum"		
		/cultivar="Greenfeast"		
		/db_xref="taxon:3888"		
gene		1..363		
CDS		/gene="DRR230"		
		56..274		
		/gene="DRR230"		
		/note="Ozone-induced, similar to the Pisum sativum cv.		
		Alaska product encoded by GenBank Accession Number L01578"		
		/codon_start=1		
		/product="disease resistance response protein 230		
		precursor"		
		/protein_id="AA043285.1"		
		/db_xref="GI:12002298"		
		/translation="MERKSLACFLLVITFIADQIVSEANTCENTLAGSYKVCFGG		
		CDRHCRFOEGALISGRCDDFRCWCTKNC"		
BASE COUNT		113 a 68 c 74 g 108 t		
ORIGIN				
		Query Match 35.8% Score 175.6; DB 8; Length 363;		
		Best Local Similarity 75.2% Pred. No. 1.2e-26;		
		Matches 245; Conservative 0; Mismatches 79; Indels 2; Gaps 2;		

OY	295	TGGATTCCTCCCA---CATCAAGTGTGCGAATGTAATGCTTTATATAAAACCTAATA	351
Db	243	TGGATTCCTCCCAACCTCAGACAACAGTGCAATGCAGGGCCATTATTAATAAACACACCA	302
OY	352	AATAAATGCACGAGTATAGCTACCAACTCATATATAT	392
Db	303	TAT-TATATATACAAATFAGCCTTCTACTGCATCATATAT	342
RESULT 7			
AB020613		496 bp	mRNA
LOCUS			linear
DEFINITION	Vigna radiata mRNA for PDI1, complete cds.		PLN 05-JAN-2002
AB020613			
AB020613.1	GI:18146787		
PDI1.			
Vigna radiata (strain:B20P5 9-3-2-2)	immature seed cDNA to mRNA,		
clone_11b:B20 clone:PDF-1.			
Vigna radiata			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;			
Vigna.			
REFERENCE			
AUTHORS	Ishimoto,M. and Kaga,A.		
TITLE	Mungbean defensin		
JOURNAL	Published Only in Database (2002)		
REFERENCE	2 (bases 1 to 496)		
AUTHORS	Ishimoto,M. and Kaga,A.		
TITLE	Direct Submission		
JOURNAL	Submitted (01-DEC-1998) Masao Ishimoto, Chugoku National Agricultural Experiment Station, Laboratory of Plant Biotechnology; 6-12-1 Nishifutatsu, Fukuyama, Hiroshima 721-8514, Japan (E-mail:ishimotoecgk.affrc.go.jp, tel:+81-849-234100(ex.231), Fax:+81-849-247893) Location/Qualifiers		
FEATURES			
source	1..496		
/organism="Vigna radiata"			
/strain="B20P5 9-3-2-2"			
/db_xref="taxon:157791"			
/clone="pdf-1"			
/tissue-type="Immature seed"			
/clone_id="B20"			
gene	1..496		
CDS	/gene="pdi1"		
46..273			
/gene="pdi1"			
/codon_start=1			
/product="PDI1"			
/protein_id="BAB82453.1"			
/db_xref="GI:18146788"			
/translation="MEKKSISLAGLCFLFLVFAQENVAVTEAKTCENLIANTIRSPCT TGSODDHCKNKKEHLRSRCRDDFCWCTRNC"			
polya_site	496		
/gene="pdi1"			
/note="17 a nucleotides"			
BASE COUNT	148 a 104 c 106 g 138 t		
ORIGIN			
Query Match	25.6%; Score 125.2; DB 8; Length 496;		
Best Local Similarity	66.7%; Pred. No. 3.3e-16;		
Matches 228; Conservative 0; Mismatches 103; Indels 11; Gaps 3;			
OY	64	CTAATCAAATGATGAGAAGAAATACATGCTGCTTTCCTCTCTTGGTTCTCT	123
Db	35	CTAATCAAGCATGAGAGGAAGAAATACATGCGCGGATTAATGCTTCCTCTCTCTCTCT	94
OY	124	TTGTTGCACAAGAAATTTGGT--GACAGAGACGAGAAACATGTGAGAAATTTGGCAGATA	180
Db	95	TTGTTGCTCAAGAAATTTGGTGGCAGATGAGGCAAAACATTTGCCAGAACTGGCGAATA	154
OY	181	AATATAGGGGACATGCTT-----TAGTGGTTGTGACACTGCATGCAACCAAGAAGA	234

Db	155	CTTACAGAGGTCATCGTTCAACA	CTGCAGCTGGCATGTGATGATCAGTCAAGAACAAGAAC	214
OY	235	ACCGACTTAGTGGAAGTGTGAGGACGACTTC	TCCGCTGCTGTACTATAAAGATTAA	294
Db	215	ACTTGAGAGAGTGCGAGGTGACGAGGACGATTTCCGGTGTGGTGCACTAGAAACGTGTAAAC		274
OY	295	TGGAATCCCTCCAATCAGTAAGTGTGCATGTGAATATGCTTATATATAAATAACTAATAAT		354
Db	275	CGGATTCCTCCCCAACCGACAAAACGTGACGACGAGGCGATTTTA--TAAATAAAAACTA		332
OY	355	AAAATGCACGAGTATAGCTACAACTTCATCTATATATATGA		396
Db	333	TATATACATACAAATAGCCTTCTACTGATATATATATGCA		374
RESULT 8				
LOCUS	PEADRR230B	456 bp	mRNA	linear
DEFINITION	Pisum sativum disease resistance response protein 39 (DRR230-b)			
ACCESSION	mRNA, complete cds.			
VERSION	L01579.88682			
KEYWORDS	L01579.1 GI:169075 cysteine-rich protein; disease resistance response protein 39; pathogenesis-related protein. Pisum sativum (strain Alaska) cDNA to mRNA. Pisum sativum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum. 1 (bases 1 to 456) Chiang,C.C. and Hadwiger,L.A. The Fusarium solani-induced expression of a pea gene family encoding high cysteine content proteins Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)			
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
MEDLINE				
PUBMED				
COMMENT				
FEATURES				
source				
gene				
CDS				
mat_peptide				
BASE COUNT				
ORIGIN				
Query Match				
Best Local Similarity				
Matches 277; Conservative				
23.3%; Score 114; DB 8; Length 456;				
61.4%; Pred. NO. 6.9e-14;				
0; Mismatches 151; Indels 23; Gaps 5;				

[illegible]

```

(TR:Q181318) BLAST Score: 378, sum P(1) = 3.8e-35; 378
identity in 297 aa overlap, predicted using hexkoon, Pfam
match to PF00076 rrm, RNA recognition motif. (a.k.a. RRM,
RBD, or RNP domain) Score 58.01"
/codon_start-1
/product-"putative RNA-binding protein"
/protein_id-"CAB39067.1"
/db_xref-"GI:4494008"
/translation-"MGLPDKIRIKLEALNEALKNIGNNDSMDHOYRDSYIYIGNDL
NLTGEGDIVVSGPEPIDVALVDRNTEGSKGCEIYADNOSTIADVNFNGYKTL
LERPLVGHILIALRLPKRTIKLDADKNKRPPIGAGQIGVYVNESEIKLSDYDKIK
NSNSKEKKKILWDEDELWALNLEKSIKIDIIISPIGHDKSRHNSGMEEEEDDEEDD
EDDDDDSDSDVYIKYRHKRKKRKSJTTKRYDKKEHKRKSJHRRHNSHREKRE
EDDDSKHRRKSHYDKYSRSRSYSTSSSDR"
join(7801..7928,8084..8234,8392..8583)
/gene-"PFC0870w", MAL3p7.3"
join(7801..7928,8084..8234,8392..8583)
/gene-"PFC0870w", MAL3p7.3"
/gene-"PFC0870w", MAL3p7.3", putative elongation factor,
len: 181 aa; Similarity to P. falciparum elongation factor
1-beta, (AA275224) (276 aa), fasta scores: Opt: 366, E):
1..1e-15, 53.2% identity in 141 aa overlap, revised:
shortened exon 2, Pfam: match to PF00736 EF1B, EF-1
guanine nucleotide exchange domain Score 61.10"
/codon_start-1
/product-"putative elongation factor"
/protein_id-"CAB39068.2"
/db_xref-"GI:8052274"
/db_xref-"SPTREMBL:O97319"
/translation-"WANTYDELVPLSYIIITQNSGNTSKIDQANTKKPKKEVYNS
SLIDIRKPGENTDLDEVILKIKNTMGLTWGKAHKTPAFGLFKLVSCVIVDD
VNTDEIETENIGLGNDELQKKOMDDDEEYVEDDEIGLVASLETISFNK"
8235..8240
/gene-"PFC0870w", MAL3p7.3"
/note-"revised splice donor sequence for exon 2 of
PFC0870w"
8580..8585
/note-"potential splice donor sequence may indicate
further splicing of PFC0870w"
join(11431..20416,20578..20690)
/gene-"PFC0875w", MAL3p7.4"
join(11431..20416,20578..20690)
/gene-"PFC0875w", MAL3p7.4"
/note-"PFC0875w", MAL3p7.4"
3032 aa, revised: added 3' exon, possibly spliced at 5'
end"
/codon_start-1
/product-"hypothetical protein, PFC0875w"
/protein_id-"CAB39024.2"
/db_xref-"GI:8052275"
/db_xref-"SPTREMBL:O97278"
/translation-"MKDPLSYAENNDLMEFKLYNSEEDCLNKIYATEIKSEDKNNW
SELDNDILNIHENDKNSLIYLNHTNITNLKSSSEPNIDILKDYTTENEPENTIKIKI
NHLILKVAANYTEFYKNFIKDILNLENNHYYQYENDDRKLFYFNFKNNLVKRYSCG
GLSHLEKVVYKQKNVFKSYFGLSPQSEGGKGLKNAPLNLYENKQYGFPHL
YXPYITLEDKRIENKERNENKERNENKERNKKEKKMEKKIDLSNNVNNYK
NGIOSHHNNSINSNDODKKNNNNNNNYYNNPGLITNTKYKILRGVDYLLNSNKK
YFNPDINIKONFNFNTNPDYSPNITFENKYYSPFIVLEQYQNSITLNYADILK
KNMLTPRIDELNEINLERETITMEKKTDEKEYOVANNYINENYIDKGGKYTELKL
LNDPFLYKPKMSKINAEDFEKNIPFVVVFLCGLFVINCIDINKERINLENELP
CGLINKYKYYYSWLFYFILLFEPYNIIFTLVAVVYVYKCLMNFILFYLIFLMS
LLETTIICMOFSNNSINYYIAPLFLFESSPLIHSASNIIFEVLLIHSSECLSS
LDFIPLIKNNIKIDYKOLFKEFNISLIMHIIISIVAFVILLIANTYIYKRRKNN
MLATKRYKSGSITNDKRRKSQKTYEGNINIDMSEKYPHOLAKNSNDPMLEGSDBD
DDTCYELDLTKKQVNSOMCLTEKIRINDRESNHPDIDMILPILRHNNNINNNINNN
INNINNNINNNINNOHRNNOCYIILONVKKFYGKHALDVSJTLASNI FVLLGEE
NCSGSTLINITTKIKISKDSGEINFEKFSYKKNKCDIYNDVKNRRKPLCGISNGS
KEFWNTRFKRNCNDTNNYDNNSSNNNNNNHNSNGINSFNNNNVANKNNI
KNDLSTYCSOAVILLENUTPEYTKITILYLYNNKVDYLLKKRTKLIMNDLIVYI
NQIKLMDVECAKISITFCPLVKRDIILIDEPFLADIKTKLKFEDKIKANNIIL
FICHDIIYEANNFADIIVAKSGIILFSGSINSPKILLESYFTNITONGNPNDEORN
YLSOIKSINALKKKVIKSPRYANNYDGVNGLISSEHSINDIKDKDNNNDNDDD

```


THIS PAGE BLANK (USPTO)

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2003, 05:54:13 ; Search time 57.7389 Seconds

(without alignments)
2602.608 Million cell updates/sec

Title: US-10-010-731-10_COPY_18_507

Sequence: 1 TGTCAACACACACATACCA.....CAAAAAAAAAAAAAAAAA 490

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 segs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*\n2: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*\n3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*\n4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*\n5: /cgn2_6/ptodata/1/ina/PCBUS.COMB.seq:*\n6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	488	99.6	490	US-09-003-198A-19	Sequence 19, Appl
2	488	99.6	507	US-08-766-355-10	Sequence 10, Appl
3	488	99.6	507	US-09-003-198A-10	Sequence 10, Appl
4	488	99.6	507	US-09-003-198A-10	Sequence 10, Appl
5	301.8	61.6	327	US-08-766-355-9	Sequence 9, Appl
6	301.8	61.6	327	US-09-003-198A-9	Sequence 9, Appl
7	301.8	61.6	327	US-09-003-198A-9	Sequence 9, Appl
8	234	47.8	250	US-08-766-355-13	Sequence 13, Appl
9	234	47.8	250	US-09-003-198A-13	Sequence 13, Appl
10	234	47.8	250	US-09-003-198A-13	Sequence 13, Appl
11	228.6	46.7	293	US-08-766-355-6	Sequence 6, Appl
12	228.6	46.7	293	US-09-003-198A-6	Sequence 6, Appl
13	228.6	46.7	293	US-09-003-198A-6	Sequence 6, Appl
14	181.2	37.0	189	US-09-003-198A-18	Sequence 18, Appl
15	179.8	36.7	200	US-08-766-355-5	Sequence 5, Appl
16	179.8	36.7	200	US-09-003-198A-5	Sequence 5, Appl
17	179.8	36.7	200	US-09-003-198A-5	Sequence 5, Appl
18	179.8	36.7	200	US-09-003-198A-5	Sequence 5, Appl
19	54	11.0	62	US-08-766-355-11	Sequence 11, Appl
20	54	11.0	62	US-09-003-198A-11	Sequence 11, Appl
21	41.4	8.4	751	US-09-428-805-11	Sequence 11, Appl
22	40	8.2	141	US-08-377-687-35	Sequence 35, Appl
23	40	8.2	141	US-08-377-687-35	Sequence 35, Appl
24	40	8.2	141	US-08-377-687-35	Sequence 35, Appl
25	39.6	8.1	7218	US-08-971-982-35	Sequence 35, Appl
26	39	8.0	47	US-08-766-355-12	Sequence 12, Appl
27	39	8.0	47	US-09-003-198A-12	Sequence 12, Appl

c	28	39	8.0	47	4	US-09-428-805-12	Sequence 12, Appl
c	29	38	7.8	860	4	US-08-998-416-287	Sequence 287, Appl
c	30	37.6	7.7	946	3	US-08-916-443A-15	Sequence 15, Appl
c	31	37.6	7.7	5852	1	US-07-867-106-2	Sequence 2, Appl
c	32	36.6	7.5	636	4	US-08-998-416-1137	Sequence 1137, Appl
c	33	36.6	7.5	6124	4	US-08-213-419B-3	Sequence 3, Appl
c	34	36.4	7.4	1872	4	US-09-291-922-27	Sequence 27, Appl
c	35	35.8	7.3	1620	3	US-08-985-950-11	Sequence 11, Appl
c	36	35.8	7.3	9636	1	US-08-323-170B-1	Sequence 1, Appl
c	37	35.8	7.3	9636	4	US-08-954-441-1	Sequence 1, Appl
c	38	35.6	7.3	3463	4	US-09-189-462-3	Sequence 1, Appl
c	39	35.4	7.2	963	4	US-09-134-001C-1367	Sequence 1367, Appl
c	40	35.4	7.2	1364	4	US-09-182-034-1	Sequence 1, Appl
c	41	35.2	7.2	1212	4	US-09-182-145-35	Sequence 34, Appl
c	42	35.2	7.2	1212	4	US-09-182-145-35	Sequence 35, Appl
c	43	35.2	7.2	33000	4	US-09-215-694-18	Sequence 18, Appl
c	44	35	7.1	427	4	US-09-438-906-31	Sequence 31, Appl
c	45	35	7.1	849	4	US-09-475-316A-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-09-003-198A-19
Sequence 19, Application US/09003198A
Patent No. 6316407
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,198A
FILING DATE: 07-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1440
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 490 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-003-198A-19

Query Match 99.6%; Score 488; DB 4; Length 490;

Best Local Similarity 100.0%; Pred. No. 1.1e-118; Indels 0; Gaps 0;

Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TGTCAACACACACATACCAATGACCGTACGATTAATTTATATATATTCATC 60

DB 1 TGTCAACACACACATTAACATTAAGTGCCTGAGTCACTTAATTAATATATATTCATC 60
QY 61 AATCTAATCAAACTATGAGAGAAATCACTAGCTGGTCTTATGCTCTCTCTTGGTTC 120
DB 61 AATCTAATCAAACTATGAGAGAAATCACTAGCTGGTCTTATGCTCTCTCTTGGTTC 120
QY 121 TCTTGTTCACAGAAATTTGTGTGACAGAAAGCCAGAAATGTGAGAAATTTGGCAGATA 180
DB 121 TCTTGTTCACAGAAATTTGTGTGACAGAAAGCCAGAAATGTGAGAAATTTGGCAGATA 180
QY 181 AATATGGGGACCATGCTTATGCTGTGTGACATCTGACATGACCAACCAAGAGAAAGCCAG 240
DB 181 AATATGGGGACCATGCTTATGCTGTGTGACATCTGACATGACCAACCAAGAGAAAGCCAG 240
QY 241 TTATGTGAAGGTGTAGGAGACACTTCCGCTGCTGTGTACTTAAATGATGTTAATGATC 300
DB 241 TTATGTGAAGGTGTAGGAGACACTTCCGCTGCTGTGTACTTAAATGATGTTAATGATC 300
QY 301 TCTTCCACATCAAGATGTGATGCAATGATGCTTTATTAATAAACTAAATTAATAATG 360
DB 301 TCTTCCACATCAAGATGTGATGCAATGATGCTTTATTAATAAACTAAATTAATAATG 360
QY 361 CACGAGTATGATCAATCTCATATATATATGATGATGATGATGATGATGATGATGATG 420
DB 361 CACGAGTATGATCAATCTCATATATATATGATGATGATGATGATGATGATGATGATG 420
QY 421 GTTATGACTTCTATCATATGGAATTAACATCAATTAATTTGCTTCCAAATTAATG 480
DB 421 GTTATGACTTCTATCATATGGAATTAACATCAATTAATTTGCTTCCAAATTAATG 480
QY 481 AAAAAAAAAA 490
DB 481 AAAAAAAAAA 490

RESULT 2
US-08-766-355-10
; Sequence 10, Application US/08766355
; Patent No. 6121436
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip Maganlal
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 77210
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,355
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MOBT:063
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:

LENGTH: 507 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: one-of(17, 424, 485)
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "N = A or C or G or T"
US-08-766-355-10

Query Match 99.6%; Score 488; DB 3; Length 507;
Best Local Similarity 100.0%; Pred. No. 1,1e-118;
Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTCAACACACACATTAACATTAAGTGCCTGAGTCACTTAATTAATATATATTCATC 60
DB 18 TGTCAACACACACATTAACATTAAGTGCCTGAGTCACTTAATTAATATATATTCATC 77
QY 61 AATCTAATCAAACTATGAGAGAAATCACTAGCTGGTCTTATGCTCTCTCTTGGTTC 120
DB 78 AATCTAATCAAACTATGAGAGAAATCACTAGCTGGTCTTATGCTCTCTCTTGGTTC 137
QY 121 TCTTGTTCACAGAAATTTGTGTGACAGAAAGCCAGAAATGTGAGAAATTTGGCAGATA 180
DB 138 TCTTGTTCACAGAAATTTGTGTGACAGAAAGCCAGAAATGTGAGAAATTTGGCAGATA 197
QY 181 AATATGGGGACCATGCTTATGCTGTGTGACATCTGACATGACCAACCAAGAGAAAGCCAG 240
DB 198 AATATGGGGACCATGCTTATGCTGTGTGACATCTGACATGACCAACCAAGAGAAAGCCAG 257
QY 241 TTATGTGAAGGTGTAGGAGACACTTCCGCTGCTGTGTACTTAAATGATGTTAATGATC 300
DB 258 TTATGTGAAGGTGTAGGAGACACTTCCGCTGCTGTGTACTTAAATGATGTTAATGATC 317
QY 301 TCTTCCACATCAAGATGTGATGCAATGATGCTTTATTAATAAACTAAATTAATAATG 360
DB 318 TCTTCCACATCAAGATGTGATGCAATGATGCTTTATTAATAAACTAAATTAATAATG 377
QY 361 CACGAGTATGATCAATCTCATATATATATGATGATGATGATGATGATGATGATGATG 420
DB 378 CACGAGTATGATCAATCTCATATATATATGATGATGATGATGATGATGATGATGATG 437
QY 421 GTTATGACTTCTATCATATGGAATTAACATCAATTAATTTGCTTCCAAATTAATG 480
DB 438 GTTATGACTTCTATCATATGGAATTAACATCAATTAATTTGCTTCCAAATTAATG 497
QY 481 AAAAAAAAAA 490
DB 498 AAAAAAAAAA 507

RESULT 3
US-09-003-198A-10
; Sequence 10, Application US/09003198A
; Patent No. 6316407
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip Maganlal
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,198A
FILING DATE: 07-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 507 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: one-of(17, 424, 485)
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "N - A or C or G or T"
US-09-003-198A-10

Query Match 99.6%; Score 488; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;
Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTCAACACACACATTAACATTAAGTACCGGAGTCATTAATTAATTAATTCATC 60
DB 18 TGTCAACACACACATTAACATTAAGTACCGGAGTCATTAATTAATTAATTCATC 77
QY 61 AATCTAATCAAACTATGAGAGAAATCACTAGCTGGCTATGCTTCTCTTGGTTC 120
DB 78 AATCTAATCAAACTATGAGAGAAATCACTAGCTGGCTATGCTTCTCTTGGTTC 137
QY 121 TCTTTGTGACAGAAGAAATGTGTGACAGAACCCAGAACATGTGAGAAATTTGGCAGATA 180
DB 138 TCTTTGTGACAGAAGAAATGTGTGACAGAACCCAGAACATGTGAGAAATTTGGCAGATA 197
QY 181 AATATGAGGAGACATGCTTTAGTGTGTGTGACACTCAGTACACCAACCAAGAGACGAG 240
DB 198 AATATGAGGAGACATGCTTTAGTGTGTGTGACACTCAGTACACCAACCAAGAGACGAG 257
QY 241 TTAGTGAAGAGGTAGGAGACACTCCGCTGCTGTGTACTTAAAGATGTTAATGATC 300
DB 258 TTAGTGAAGAGGTAGGAGACACTCCGCTGCTGTGTACTTAAAGATGTTAATGATC 317
QY 301 TCTTCCACATCAAGATGTGCATGGAATAGCTTTTATTAATAAACTAAATAATTAATG 360
DB 318 TCTTCCACATCAAGATGTGCATGGAATAGCTTTTATTAATAAACTAAATAATTAATG 377
QY 361 CAGGAGTATAGTACAACTTCACTATATATATGACTCAATTCGNGCATTAAGTATTA 420
DB 378 CAGGAGTATAGTACAACTTCACTATATATATGACTCAATTCGNGCATTAAGTATTA 437
QY 421 GTATACACTCTATCATATGAAATAAATCAATTAATTAATTCGNTCCAAAAAAA 480
DB 438 GTATACACTCTATCATATGAAATAAATCAATTAATTAATTCGNTCCAAAAAAA 497
QY 481 AAAAAAAAAA 490
DB 498 AAAAAAAAAA 507

RESULT 4
US-09-428-805-10
; Sequence 10, Application US/09428805
; Patent No. 6329504

GENERAL INFORMATION:

APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakim, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
CONTROLLING PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 77210
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/428,805
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/766,355
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT:063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 507 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: one-of(17, 424, 485)
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "N - A or C or G or T"
US-09-428-805-10

Query Match 99.6%; Score 488; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;
Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTCAACACACACATTAACATTAAGTACCGGAGTCATTAATTAATTAATTCATC 60
DB 18 TGTCAACACACACATTAACATTAAGTACCGGAGTCATTAATTAATTAATTCATC 77
QY 61 AATCTAATCAAACTATGAGAGAAATCACTAGCTGGCTATGCTTCTCTTGGTTC 120
DB 78 AATCTAATCAAACTATGAGAGAAATCACTAGCTGGCTATGCTTCTCTTGGTTC 137
QY 121 TCTTTGTGACAGAAGAAATGTGTGACAGAACCCAGAACATGTGAGAAATTTGGCAGATA 180
DB 138 TCTTTGTGACAGAAGAAATGTGTGACAGAACCCAGAACATGTGAGAAATTTGGCAGATA 197
QY 181 AATATGAGGAGACATGCTTTAGTGTGTGTGACACTCAGTACACCAACCAAGAGACGAG 240
DB 198 AATATGAGGAGACATGCTTTAGTGTGTGTGACACTCAGTACACCAACCAAGAGACGAG 257
QY 241 TTAGTGAAGAGGTAGGAGACACTCCGCTGCTGTGTACTTAAAGATGTTAATGATC 300
DB 258 TTAGTGAAGAGGTAGGAGACACTCCGCTGCTGTGTACTTAAAGATGTTAATGATC 317
QY 301 TCTTCCACATCAAGATGTGCATGGAATAGCTTTTATTAATAAACTAAATAATTAATG 360

Db	318	TCCTCAACATCAAGATGTGCATGGAATAGTCTTTATATATAAACTAATAATAATAAATG	3777
Qy	361	CACGCAAGTATGTACAAACCTCATCTATATATATAGACTCATATACGCGCATTAAGCTTTA	4202
Db	378	CACGAGATATAGCTACAACTTCATCTATATATATATAGACTCAATATCGCGCATTAACGTTTA	4377
Qy	421	GTTATGCACTTCATTCATATGGAATAAACAATCAATAAGTAAATTCGTTCCAAAAA	4808
Db	438	GTTATGCACTTCATTCATATGGAATAAACAATCAATAAGTAAATTCGTTCCAAAAA	4977
Qy	481	AAAAAAAAA 490	
Db	498	AAAAAAAAA 507	

RESULT 5
 US-08-766-355-9
 Sequence 9, Application US/08766355
 Patent No. 6121436
 GENERAL INFORMATION:
 APPLICANT: Liang, Jihong
 APPLICANT: Shah, Dilip Maganlal
 APPLICANT: Wu, Yonnie S.
 APPLICANT: Rosenberger, Cindy A.
 APPLICANT: Hakimi, Salim
 TITLE OF INVENTION: Antifungal Polypeptide and Methods for
 TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 77210
 CITY: Houston
 STATE: Texas
 COUNTRY: United States of America
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/766,355
 FILING DATE: Concurrently Herewith
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Kitchell, Barbara S.
 REGISTRATION NUMBER: 33,928
 REFERENCE/DOCKET NUMBER: MORF:063
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (512) 474-7577
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 327 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: modified_base
 LOCATION: one-of(244, 305)
 OTHER INFORMATION: /mod_base-OTHER
 OTHER INFORMATION: /note="N = A or C or G or T"
 US-08-766-355-9

Query Match	91.6%	Score 301.8	DB 3	Length 327
Best Local Similarity	97.6%	Pred. No. 3,7	70	
Matches	319	Conservative	0	Mismatches 7
				Indels 1
				Gaps 1
Qy	165	GAGAAATGGCGCAGATAAATATATGAGGGGACCACTGCTTACTGCTGTGGACACTACTGCGACA	224	
Db	1	GAGAAATGGCGCGATTAAGCTATAGGGGACCACTGCTTACTGCTGTGGACACTACTGCGACA	60	

Oy	225	ACCAAAGGAACGAGTAGTGGGAAGGTGTGGGACACATTCGCGTCTGGTACTAAA	284
Db	61	ACCAAAGGAACGAGTAGTGGGAAGGTGTGGGATTCGCTGGTACTAAA	120
Oy	285	AGATGTTAAATGATCTCTCCACACATCAGATGTGCATGGATAGTCTTTATATATAAA	344
Db	121	AGATGTTAAATGATCTCTCCACACATCAGATGTGCATGGATAGTCTTTATATATAAA	180
Oy	345	CTAAATATAATATAATGACGACGATATAGTCTCAACTCATCTATATATATG-ACTCATA	403
Db	181	CTAAATATAATATAATGACGACGATATAGTCTCAACTCATCTATATATATGACTCATTA	240
Oy	404	TCGNCATTAACGTTATAGTTATGCACCTTCTATCATATATGAAATAAACATCAATAAGTAAT	463
Db	241	TCGNCATTAACGTTATAGTTATGCACCTTCTATCATATATGAAATAAACATCAATAAGTAAT	300
Oy	464	TCGTTCCAAAAAAAAAAAAAAAAAAAAAA	490
Db	301	TCGTTCCAAAAAAAAAAAAAAAAAAAAAA	327

```

RESULT 6
US-09-003-198A-9
: Sequence 9, Application US/09003198A
: Patent No. 6316407
: GENERAL INFORMATION:
: APPLICANT: Liang, Jihong
: APPLICANT: Shah, Dilip Maganlal
: APPLICANT: Wu, Yonnie S.
: APPLICANT: Rosenberger, Cindy A.
: APPLICANT: Hakimi, Salim
: TITLE OF INVENTION: Antifungal Polypeptide and Methods for
: TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold White & Durkee
: STREET: P. O. Box 4433
: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/003,198A
: FILING DATE: 07-JAN-1998
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Patterson, Melinda L.
: REGISTRATION NUMBER: 33,062
: REFERENCE/DOCKET NUMBER: MOBT.193
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (713) 787-1400
: TELEFAX: (713) 787-1440
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 327 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: modified_base
: LOCATION: one-of(244, 305)
: OTHER INFORMATION: /mod_base= OTHER
: OTHER INFORMATION: /note="N - A or C or G or T"
US-09-003-198A-9

```

Query Match	61.6%	Score 301.8	DB 4	Length 327
Best Local Similarly	97.6%	Pred. No. 3.7e-70		
Matches 319; Conservative	0	Mismatches 7	Indels 1	Gaps 1

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-766-355-13

Query Match 47.8%; Score 234; DB 3; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.7e-52;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 CAATCTAATCAAACTATGAGAGAAATCACTAGCTGCTTATGCTTCCCTCTTGTT 119
DB 9 CAATCTAATCAAACTATGAGAGAAATCACTAGCTGCTTATGCTTCCCTCTTGTT 68
QY 120 CTCCTTTGTCACAGAAATTTGGTGACAGAACCAATGTGAAATTTGGCAGAT 179
DB 69 CTCCTTTGTCACAGAAATTTGGTGACAGAACCAATGTGAAATTTGGCAGAT 128
QY 180 AAATATAGGGGACCACTTATGCTTGTGACACTGACACACCAAGAGACGCA 239
DB 129 AAATATAGGGGACCACTTATGCTTGTGACACTGACACACCAAGAGACGCA 188
QY 240 GTTAGTGAAGGTGTAGGAGACGACTCCGCTGCTGTACTAAAGATGTAA 293
DB 189 GTTAGTGAAGGTGTAGGAGACGACTCCGCTGCTGTACTAAAGATGTAA 242

RESULT 9

US-09-003-198A-13
Sequence 13, Application US/09003198A
Patent No. 6316407

GENERAL INFORMATION:

APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal polypeptide and Methods for
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,198A
FILING DATE: 07-JAN-1998
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MORT:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-003-198A-13

Query Match 47.8%; Score 234; DB 4; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.7e-52;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 CAATCTAATCAAACTATGAGAGAAATCACTAGCTGCTTATGCTTCCCTCTTGTT 119
DB 9 CAATCTAATCAAACTATGAGAGAAATCACTAGCTGCTTATGCTTCCCTCTTGTT 68
QY 120 CTCCTTTGTCACAGAAATTTGGTGACAGAACCAATGTGAAATTTGGCAGAT 179
DB 69 CTCCTTTGTCACAGAAATTTGGTGACAGAACCAATGTGAAATTTGGCAGAT 128
QY 180 AAATATAGGGGACCACTTATGCTTGTGACACTGACACACCAAGAGACGCA 239
DB 129 AAATATAGGGGACCACTTATGCTTGTGACACTGACACACCAAGAGACGCA 188
QY 240 GTTAGTGAAGGTGTAGGAGACGACTCCGCTGCTGTACTAAAGATGTAA 293
DB 189 GTTAGTGAAGGTGTAGGAGACGACTCCGCTGCTGTACTAAAGATGTAA 242

RESULT 10

US-09-428-805-13
Sequence 13, Application US/09428805
Patent No. 6329504

GENERAL INFORMATION:

APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal polypeptide and Methods for
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 77210
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/428,805
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/766,355
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MORT:063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-428-805-13

Query Match 47.8%; Score 234; DB 4; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.7e-52;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 CAATCTAATCAAACTATGAGAGAAATCACTAGCTGCTTATGCTTCCCTCTTGTT 119
DB 9 CAATCTAATCAAACTATGAGAGAAATCACTAGCTGCTTATGCTTCCCTCTTGTT 68

QY	1	TGTTAAACACACATATAACATTAAGTACCGTGAGTCATTAAATTTATATATATTCATC	60
Dy	18	TGTTAAACACACACATATAACATTAAGTACCGTGAGTCATTAAATTTATATATTCATC	77
QY	61	AATCTAATCAAACTAGTGAGAGAATACTAGCTGGCTATATGCTTCCTCTTGGTTC	120
Dy	78	AATCTAATCAAACTAGTGAGAGAATACTAGCTGGCTATATGCTTCCTCTTGGTTC	137

	Matches	246;	Conservative	0;	Mismatches	30;	Indels	0;	Gaps
QY	1	TGTCAACACACACATTAACACATTAAGTACCGGTAGTCATTAATTAATTAATTCATC	60						
Db	18	TGTCAACACACACATTAACACATTAAGTACCGGTAGTCATTAATTAATTAATTCATC	77						
QY	61	AATCTAATCAAAAGTATGTAGAGAAATCACTAGCTGTGCTTATGCTTCTCTTCCTGGTTC	120						

Db 78 ATCTAATCAACATGAGAGAAATCACTAGCTGCTTATGCTTCTCTCTC 137
QY 121 TCTTTGTGCAAGAAATTTGTGTCAGAGACCCAGACATGTGAGAAATTTGGCAGATA 180
Db 138 TCTTTGTGCAAGAAATTTATGTCAGCAGCAGCTACTGTGAGAAATTTGGCTAACA 197
QY 181 AATATAGGGAGCATTGCTTGTAGTGTGTGACACTGACACCAACCAAGAGACGAC 240
Db 198 CATACAGGGAGCATTGCTTGTGTCAGCTTTCAGCTGCAAAACCAAGAACTTAC 257
QY 241 TTAGTGAAGGTGTAGGAGCAGACTTCGCTGTGT 276
Db 258 TTAGCGGNAGTGTGAGGAGCAGACTTCGCTGTGT 293

RESULT 13
US-09-428-805-6
; Sequence 6, Application US/09428805
; Patent No. 6329504
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
NUMBER OF SEQUENCES: 14
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 77210
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/428,805
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/766,355
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT:063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified base
LOCATION: one-of(117, 265)
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "N = A or C or G or T"

US-09-428-805-6

Query Match 46.7%; Score 228.6; DB 4; Length 293;
Best Local Similarity 89.1%; Pred. No. 4.5e-51;
Matches 246; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1 TGTCAACACACATTAACATTAAGTACCGTACATTAATTAATATATATTC 60
|||||

Db 18 TGTCAACACACACATTAACATTAAGTACCGTACATTAATTAATATATTC 77
QY 61 ATCTAATCAACATGAGAGAAATCACTAGCTGCTTATGCTTCTCTCTG 120
Db 78 ATCTAATCAACATGAGAGAAATCACTAGCTGCTTATGCTTCTCTCTG 137
QY 121 TCTTTGTGCAAGAAATTTGTGTCAGAGACCCAGACATGTGAGAAATTTGGCAGATA 180
Db 138 TCTTTGTGCAAGAAATTTATGTCAGCAGCAGCTACTGTGAGAAATTTGGCTAACA 197
QY 181 AATATAGGGAGCATTGCTTGTAGTGTGTGACACTGACACCAACCAAGAGACGAC 240
Db 198 CATACAGGGAGCATTGCTTGTGTCAGCTTTCAGCTGCAAAACCAAGAACTTAC 257
QY 241 TTAGTGAAGGTGTAGGAGCAGACTTCGCTGTGT 276
Db 258 TTAGCGGNAGTGTGAGGAGCAGACTTCGCTGTGT 293

RESULT 14
US-09-003-198A-18
; Sequence 18, Application US/09003198A
; Patent No. 6316407
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
NUMBER OF SEQUENCES: 19
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,198A
FILING DATE: 07-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

US-09-003-198A-18

Query Match 37.0%; Score 181.2; DB 4; Length 189;
Best Local Similarity 98.4%; Pred. No. 9.2e-39;
Matches 183; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 94 CTGCTTATGCTTCTCTCTTGTGTCAGACAGAAATTTGTGTCAGAG 153
Db 1 CAGGCTTATGCTTCTCTCTTGTGTCAGACAGAAATTTGTGTCAGAG 60
|||||

QY 154 CCAAGACATGTGAGAAATTTGCGACATTAATTAAGGAGCAGCTTGTAGTGTGACA 213
|||||

Db	61	CCAAACAATGTGAGAAATTTGGCAATAAATATATAGGGACCATGCTTTAGTGGTTGTGACA	120
Qy	214	CTCACTGCACAAACCAAGAGAGAACGACATTTAGTGAAGGTGAGACACTTCGCGTGT	273
Db	121	CTCACTGCACAAACCAAGAGAACGACATTTAGTGAAGGTGAGGACACTTCGCTGCT	180
Qy	274	GCTGTA	279
Db	181	GCTGGA	186

```

Db      138  CTCACCTGCACACCAAGAGAACCCAGTTAGTGGAGGTGTAGGAGACACTTCCCGCTCT 197
          |||
Qy      274  GGT  276
          |  |
Db      198  GCT  200

```

Search completed: May 8, 2003, 07:20:52
Job time : 60.7389 secs

Search completed: May 8, 2003, 07:20:52
Job time : 60.7389 secs

RESULT 15
 US-08-766-355-5
 Sequence 5, Application US/08766355
 Patent No. 6121436
 GENERAL INFORMATION:
 APPLICANT: Liang, Jihong
 APPLICANT: Shah, Dilip Maganlal
 APPLICANT: Wu, Yonnie S.
 APPLICANT: Rosenberger, Cindy A.
 APPLICANT: Hakimi, Salim
 TITLE OF INVENTION: Antifungal Polypeptide and Methods for
 TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 77210
 CITY: Houston
 STATE: Texas
 COUNTRY: United States of America
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/766,355
 FILING DATE: Concurrently Herewith
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Kitchell, Barbara S.
 REGISTRATION NUMBER: 33,928
 REFERENCE/DOCKET NUMBER: MOBN:063
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (512) 474-7577
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 200 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: modified_base
 LOCATION: 17
 OTHER INFORMATION: /mod_base- OTHER
 OTHER INFORMATION: /note= "N = A or C or G or T"
 US-08-766-355-5

THIS PAGE BLANK (USPTO)

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2003, 05:48:03 ; Search time 161.513 seconds
(Without alignments)
3770.139 Million cell updates/sec

Title: US-10-010-731-10_COPY_18_507
Perfect score: 490
Sequence: 1 TGTCAACACACACATACCA.....CAAAAAAAAAAAAAAAAAAAAA 490

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 783854 seqs, 621352466 residues

Total number of hits satisfying chosen parameters: 1567708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	488	99.6	490	9	US-10-010-731-19
2	488	99.6	507	9	US-10-010-731-10
3	301.8	61.6	327	9	US-10-010-731-9
4	234	47.8	250	9	US-10-010-731-13
5	228.6	46.7	293	9	US-10-010-731-6
6	181.2	37.0	189	9	US-10-010-731-18
7	179.8	36.7	200	9	US-10-010-731-5
8	127.4	26.0	494	9	US-09-805-694B-5
9	127.4	26.0	563	9	US-10-178-213-439
10	95.2	19.4	464	9	US-10-178-213-379
11	93.2	19.0	420	9	US-10-178-213-436
12	93	19.0	461	9	US-10-178-213-451
13	54	11.0	62	9	US-10-010-731-11
14	49.6	10.1	338	9	US-10-178-213-427
15	44.4	9.1	640681	10	US-09-790-988-1
16	44.2	9.0	438	9	US-10-178-213-418
17	44.2	9.0	455	9	US-10-178-213-415
18	44.2	9.0	9515	9	US-10-239-676-160
19	44	9.0	293	9	US-10-178-213-421

c 20	42.6	8.7	5689	9	US-10-239-676-90	Sequence 90, App1
c 21	41.8	8.5	7544	9	US-10-239-676-5	Sequence 5, App1
c 22	41.4	8.4	12968	9	US-10-239-676-202	Sequence 202, App
c 23	40.6	8.3	6815	9	US-10-239-676-50	Sequence 50, App1
c 24	40.2	8.2	8588	9	US-10-239-676-178	Sequence 178, App
c 25	40.2	8.2	17419	9	US-10-239-676-99	Sequence 99, App1
c 26	40	8.2	141	10	US-09-759-584-35	Sequence 35, App1
c 27	40	8.2	211	10	US-09-960-352-2195	Sequence 2195, Ap
c 28	39.8	8.1	215	9	US-10-060-036-2168	Sequence 2168, Ap
c 29	39.8	8.1	8801	9	US-10-239-676-144	Sequence 144, App
c 30	39.8	8.1	9293	9	US-10-239-676-25	Sequence 25, App1
c 31	39.8	8.1	17142	9	US-10-239-676-206	Sequence 206, App
c 32	39.6	8.1	11260	9	US-10-239-676-19	Sequence 19, App1
c 33	39.4	8.0	479	10	US-09-960-352-12872	Sequence 12872, A
c 34	39.2	8.0	7810	9	US-10-239-676-142	Sequence 142, App
c 35	39.2	8.0	11812	9	US-10-239-676-210	Sequence 210, App
c 36	39	8.0	47	9	US-10-010-731-12	Sequence 12, App1
c 37	39	8.0	8866	9	US-10-239-676-139	Sequence 139, App
c 38	38.4	7.8	2000	9	US-09-938-842A-2900	Sequence 2900, App
c 39	38.4	7.8	5689	9	US-10-239-676-89	Sequence 89, App1
c 40	38.2	7.8	9539	9	US-10-239-676-52	Sequence 52, App1
c 41	38.2	7.8	17848	9	US-10-239-676-28	Sequence 28, App1
c 42	38	7.8	431	10	US-09-960-352-5558	Sequence 5558, Ap
c 43	38	7.8	1622	9	US-09-938-842A-4417	Sequence 4417, Ap
c 44	38	7.8	15649	9	US-10-239-676-103	Sequence 103, App
c 45	37.8	7.7	236	9	US-09-991-936-1213	Sequence 1213, Ap

ALIGNMENTS

RESULT 1
US-10-010-731-19
Sequence 19, Application US/10010731
Publication No. US20030041347A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip Maganlal
Wu, Yonnie S.
Rosenberger, Cindy A.
Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,731
FILING DATE: 13-No. US20030041347A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/003,198
FILING DATE: 07-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT-193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 490 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-010-731-19

Query Match 99.6%; Score 488; DB 9; Length 490;
Best Local Similarity 100.0%; Pred. No. 2.3e-114;
Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGTCAACACACACATACATACATAGTACCTGAGTCTTAAATTTATATATATTCATC 60
DB 1 TGTCAACACACACATACATACATAGTACCTGAGTCTTAAATTTATATATATTCATC 60
OY 61 AATCTAATCAACTATGAGAGAAATACATAGTCTGCTTATGCTTCCCTCTTGCTTC 120
DB 61 AATCTAATCAACTATGAGAGAAATACATAGTCTGCTTATGCTTCCCTCTTGCTTC 120
OY 121 TCTTTGTTGCACAGAAATTTGTTGTCAGAGAACCAATGTAGATTTGGCAGATA 180
DB 121 TCTTTGTTGCACAGAAATTTGTTGTCAGAGAACCAATGTAGATTTGGCAGATA 180
OY 181 AATATAGGGGACCATGCTTACTAGTGTGACACATCAGCACAACCAAGACGCG 240
DB 181 AATATAGGGGACCATGCTTACTAGTGTGACACATCAGCACAACCAAGACGCG 240
OY 241 TTAGTGGAAGGTGTAGGGACGACTCCGCTGCTGCTGCTACTAAAGATTTAAATGATC 300
DB 241 TTAGTGGAAGGTGTAGGGACGACTCCGCTGCTGCTGCTACTAAAGATTTAAATGATC 300
OY 301 TCTCTCAACATCAATGTCATGTCATGTCATTTATATATTAATTAATTAATGATC 360
DB 301 TCTCTCAACATCAATGTCATGTCATGTCATTTATATATTAATTAATTAATGATC 360
OY 361 CACGAGATAGCTCAACTTCACTATATATATGATCAATATGNGCATTAACGATTA 420
DB 361 CACGAGATAGCTCAACTTCACTATATATATGATCAATATGNGCATTAACGATTA 420
OY 421 GTTATGCACTTCTATCATATGGAATTAACATCAATAGTAATTTGTCCTCAAAAAA 480
DB 421 GTTATGCACTTCTATCATATGGAATTAACATCAATAGTAATTTGTCCTCAAAAAA 480
OY 481 AAAAAAAAAA 490
DB 481 AAAAAAAAAA 490

RESULT 2

US-10-010-731-10
Sequence 10, Application US/10010731
Publication No. US20030041347A1
GENERAL INFORMATION:

APPLICANT: Liang, Jihong
Shah, Dilip Maganlal
Wu, Yonnie S.
Rosenberger, Cindy A.
Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/010,731
FILING DATE: 13-NO. US20030041347A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/003,198
FILING DATE: 07-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 507 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified base
LOCATION: one-of(17, 424, 485)
OTHER INFORMATION: /mod_base- OTHER
/note- 'N' - A or C or G or T'
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-010-731-10

Query Match 99.6%; Score 488; DB 9; Length 507;
Best Local Similarity 100.0%; Pred. No. 2.3e-114;
Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGTCAACACACACATACATACATAGTACCTGAGTCTTAAATTTATATATATTCATC 60
DB 18 TGTCAACACACACATACATACATAGTACCTGAGTCTTAAATTTATATATATTCATC 77
OY 61 AATCTAATCAACTATGAGAGAAATACATAGTCTGCTTATGCTTCCCTCTTGCTTC 120
DB 78 AATCTAATCAACTATGAGAGAAATACATAGTCTGCTTATGCTTCCCTCTTGCTTC 137
OY 121 TCTTTGTTGCACAGAAATTTGTTGTCAGAGAACCAATGTAGATTTGGCAGATA 180
DB 138 TCTTTGTTGCACAGAAATTTGTTGTCAGAGAACCAATGTAGATTTGGCAGATA 197
OY 181 AATATAGGGGACCATGCTTACTAGTGTGACACATCAGCACAACCAAGACGCG 240
DB 198 AATATAGGGGACCATGCTTACTAGTGTGACACATCAGCACAACCAAGACGCG 257
OY 241 TTAGTGGAAGGTGTAGGGACGACTCCGCTGCTGCTGCTACTAAAGATTTAAATGATC 300
DB 258 TTAGTGGAAGGTGTAGGGACGACTCCGCTGCTGCTGCTACTAAAGATTTAAATGATC 317
OY 301 TCTCTCAACATCAATGTCATGTCATGTCATTTATATATTAATTAATTAATGATC 360
DB 318 TCTCTCAACATCAATGTCATGTCATGTCATTTATATATTAATTAATTAATGATC 377
OY 361 CACGAGATAGCTCAACTTCACTATATATATGATCAATATGNGCATTAACGATTA 420
DB 378 CACGAGATAGCTCAACTTCACTATATATATGATCAATATGNGCATTAACGATTA 437
OY 421 GTTATGCACTTCTATCATATGGAATTAACATCAATAGTAATTTGTCCTCAAAAAA 480
DB 438 GTTATGCACTTCTATCATATGGAATTAACATCAATAGTAATTTGTCCTCAAAAAA 497
OY 481 AAAAAAAAAA 490
DB 498 AAAAAAAAAA 507

RESULT 3

US-10-010-731-9
Sequence 9, Application US/10010731
Publication No. US20030041347A1
GENERAL INFORMATION:

APPLICANT: Liang, Jihong
Shah, Dilip Maganlal
Wu, Yonnie S.
Rosenberger, Cindy A.
Hakimi, Salim

TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,731
FILING DATE: 13-NO. US20030041347A1-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/003,198
FILING DATE: 07-JAN-1998

ATTORNEY/AGENT INFORMATION:
NAME: Paterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT:193

TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 327 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

FEATURE:
NAME/KEY: modified_base
LOCATION: one-of(244, 305)
OTHER INFORMATION: /mod_base= OTHER
/note= "N = A or C or G or T"

SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-010-731-9

Query Match 61.6%; Score 301.8; DB 9; Length 327;
Best Local Similarity 97.6%; Pred. No. 3.6e-67;
Matches 319; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 165 GAGATTGGCAGATTAATATAGGGGACCATGCTTGTGTTGACACTGCACACA 224
|||||
DB 1 GAGATTGGGGAATAATATAGGGGACCATGCTTGTGTTGACACTGCACACA 60
|||||

QY 225 ACCAAGAGAACGCGATTAGTGAAGGTGAAGGACGACTCCGCTGCTGTTACTAAA 284
|||||
DB 61 ACCAAGAGAACGCGATTAGTGAAGGTGAAGGACGACTCCGCTGTTACTAAA 120
|||||

QY 285 AGATGTTAAATGATCTCCCAACATCAAGATGTCATGGAATGCTTTATATATAAA 344
|||||
DB 121 AGATGTTAAATGATCTCCCAACATCAAGATGTCATGGAATGCTTTATATATAAA 180
|||||

QY 345 CTAATAATAATAATGACGCGAGTATAGCTCAACTCATCTATATATATG-ACTCAATA 403
|||||
DB 181 CTAATAATAATAATGACGCGAGTATAGCTCAACTCATCTATATATATGACTCAATA 240
|||||

QY 404 TCGNGCRAAGCATATGATGACCTCTATCATATGGAATAAACATCAATAGTAATT 463
|||||
DB 241 TCGNGCRAAGCATATGATGACCTCTATCATATGGAATAAACATCAATAGTAATT 300
|||||

QY 464 TCGTNTCCAAAAA 490

DB 301 TCGTNTCCAAAAA 327
|||||

RESULT 4
US-10-010-731-13
Sequence 13, Application US/10010731
Publication NO. US20030041347A1

GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip Maganlal
Wu, Yonnie S.
Rosenberger, Cindy A.
Hakimi, Salim

TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,731
FILING DATE: 13-NO. US20030041347A1-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/003,198
FILING DATE: 07-JAN-1998

ATTORNEY/AGENT INFORMATION:
NAME: Paterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT:193

TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-010-731-13

Query Match 47.8%; Score 234; DB 9; Length 250;
Best Local Similarity 100.0%; Pred. No. 5.1e-50;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 CAATCTAATCAAACTATGAGAGAGAAATCATTAGCTGCTTATGCTTCTCTTGTGTT 119
|||||
DB 9 CAATCTAATCAAACTATGAGAGAGAAATCATTAGCTGCTTATGCTTCTCTTGTGTT 68
|||||

QY 120 CTCCTTTGTTGCAAGAAATTTGTTGTTGACAGAGGACCAACATGTGAGAAATTTGGCAGAT 179
|||||
DB 69 CTCCTTTGTTGCAAGAAATTTGTTGTTGACAGAGGACCAACATGTGAGAAATTTGGCAGAT 128
|||||

QY 180 AAATATAGGAGCAGCTGCTTTAGTGTGTGACACTCACTGCACAAACCAAGAGACGA 239
|||||
DB 129 AAATATAGGAGCAGCTGCTTTAGTGTGTGACACTCACTGCACAAACCAAGAGACGA 188
|||||

QY 240 GTTACTGGAAGGTGAGGAGCAGCTTCGCTGCTGCTGTTACTTAAAGATGTTAA 293
|||||
DB 189 GTTACTGGAAGGTGAGGAGCAGCTTCGCTGCTGCTGTTACTTAAAGATGTTAA 242
|||||


```

; Publication No. US20030041348A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; FILE REFERENCE: 35718/246703
; CURRENT FILING DATE: 2002-06-21
; PRIOR FILING DATE: 2001-06-22
; PRIOR FILING DATE: 2001-06-22
; PRIOR FILING DATE: 2001-06-22
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 439
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Cyamopsis tetragonoloba
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (106)...(333)
; FEATURE:
; NAME/KEY: mat.peptide
; LOCATION: (190)...(330)
US-10-178-213-439

```

```

Query Match      26.0%; Score 127.4; DB 9; Length 563;
Best Local Similarity 65.9%; Pred. No. 8.8e-23;
Matches 234; Conservative 0; Mismatches 111; Indels 10; Gaps 3;

```

```

OY 50 ATATATCATCATCTAATCAAACTAGTGAAGAGAAATCACTAGCTGCTTATGCTTCT 109
    |||||
DB 81 ATTAATTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCT 140
    |||||
OY 110 CTCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 166
    |||||
DB 141 CTCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 200
    |||||
OY 167 GAATTTGGCAGTAATAATAGGGGACATGCTT-----TAGTGTGTGACACTGACTG 220
    |||||
DB 201 GAGTGTGCGACAGCATACATACAGGGGACCTGTTTACAGATGCTGCTGCTGCTGCTG 260
    |||||
OY 221 CACAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 280
    |||||
DB 261 CAGAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 320
    |||||
OY 281 TAAAGATGTTAAATGATGCTC-CTCCCAACATCAAGATGTCAGATGATGCTTATTA 339
    |||||
DB 321 CAGAAAGCTTAAATGCTGACCTTCCCTCCTCAAGATGATGATGATGATGATGATGAT 380
    |||||
OY 340 TAAAGATGTTAAATGATGCTC-CTCCCAACATCAAGATGTCAGATGATGCTTATTA 394
    |||||
DB 381 ATTAATTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCT 435
    |||||

```

```

RESULT 10
US-10-178-213-379
; Sequence 379; Application US/10178213
; Publication No. US20030041348A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert

```

```

; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; FILE REFERENCE: 35718/246703
; CURRENT FILING DATE: 2002-06-21
; PRIOR FILING DATE: 2001-06-22
; PRIOR FILING DATE: 2001-06-22
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 379
; LENGTH: 464
; TYPE: DNA
; ORGANISM: Cyamopsis tetragonoloba
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32)...(256)
; FEATURE:
; NAME/KEY: mat.peptide
; LOCATION: (116)...(253)
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1, 2
; OTHER INFORMATION: n = A,T,C or G
US-10-178-213-379

```

```

Query Match      19.4%; Score 95.2; DB 9; Length 464;
Best Local Similarity 61.8%; Pred. No. 1.2e-14;
Matches 225; Conservative 0; Mismatches 123; Indels 16; Gaps 4;

```

```

OY 50 ATATATCATCATCTAATCAAACTAGTGAAGAGAAATCACTAGCTGCTTATGCTTCT 109
    |||||
DB 7 ATTAATTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCT 66
    |||||
OY 110 CTCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 166
    |||||
DB 67 CTCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 126
    |||||
OY 167 GAATTTGGCAGTAATAATAGGGGACATGCTT-----GTGTTGTGACACTGACTG 220
    |||||
DB 127 GAGTGTGCGACAGCATACATACAGGGGACCTGTTTACAGATGCTGCTGCTGCTGCTG 186
    |||||
OY 221 CACAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 280
    |||||
DB 187 CAGAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
    |||||
OY 281 TAAAGATGTTAAATGATGCTC-CTCCCAACATCAAGATGTCAGATGATGCTTATTA 340
    |||||
DB 244 CAGAAAGCTTAAATGATGCTC-CTCCCAACATCAAGATGTCAGATGATGCTTATTA 299
    |||||
OY 341 AAAAGATGTTAAATGATGCTC-CTCCCAACATCAAGATGTCAGATGATGCTTATTA 400
    |||||
DB 300 TTATTAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 359
    |||||
OY 401 ATAT 404
    |||
DB 360 TTAT 363
    |||

```

```

RESULT 11
US-10-178-213-436
; Sequence 436; Application US/10178213
; Publication No. US20030041348A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert

```

```
APPLICANT: Herrmann, Rafael
APPLICANT: Wong, James
TITLE OF INVENTION: Defensin Polynucleotides and Methods of
FILE REFERENCE: 35718/246703
CURRENT APPLICATION NUMBER: US/10/178,213
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: 60/300,152
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/300,241
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 436
LENGTH: 420
TYPE: DNA
ORGANISM: Cyamopsis tetragonoloba
FEATURE:
NAME/KEY: CDS
LOCATION: (31)...(264)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (118)...(261)
US-10-178-213-436
```

```
Query Match          19.0%; Score 93.2; DB 9; Length 420;
Best Local Similarity 70.3%; Pred. No. 3.7e-14;
Matches 113; Conservative 0; Mismatches 58; Indels 15; Gaps 3;
```

```
QY 65 TAATCAACATGATGAGAGAAATCACTAGCTGCTTATGCTTCTC---TTCTTGTTCT 121
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21 TAAGTAATATGAGAGAAATCACTAGCTGCTTATGCTTCTCCTCATGCTGTTGT 80

QY 122 CTTTGTTCAGAAATTTGTGTG---ACAGAACCCAGAAATGAGATTGGCAGA 178
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 81 GTTAGTTGCGAAGAGTAGTGGTGAACAGAGGGAACAGATGAGAACTTTCGAGA 140

QY 179 TAAATATAGGGGACATGCTTTAGTG-----GTTGACACCTACGCAACACAA 229
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 141 TCAATTCAGGGGTCCATGCTTCCCTGAGACCGCCAGCATGACAGACAA 200

QY 230 AGAGAACGAGTATGAGAGAGTGTAGGAGCAGACTTCCGCTGCTGTACTAAAGATG 289
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 201 AGAGCACTTCTCAGCGGAGAGGTGACAGACGATTTTCGCTGCTGCGACCAAAACTG 260

QY 290 TTAAT 295
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 261 TTAAT 266
```

```
RESULT 12
US-10-178-213-451
; Sequence 451, Application US/10178213
; Publication No. US20030041348A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harveil, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
TITLE OF INVENTION: Defensin Polynucleotides and Methods of
FILE REFERENCE: 35718/246703
CURRENT APPLICATION NUMBER: US/10/178,213
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: 60/300,152
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/300,241
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 469
```

```
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 451
LENGTH: 461
TYPE: DNA
ORGANISM: Arachis hypogaea
FEATURE:
NAME/KEY: CDS
LOCATION: (44)...(271)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (128)...(268)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 305, 319, 357, 372, 400, 406, 420, 443, 452, 455
OTHER INFORMATION: n = A,T,C or G
US-10-178-213-451
```

```
Query Match          19.0%; Score 93; DB 9; Length 461;
Best Local Similarity 68.5%; Pred. No. 4.3e-14;
Matches 161; Conservative 0; Mismatches 65; Indels 9; Gaps 2;
```

```
QY 70 AAATATGAGAGAAATCACTAGCTGCTTATGCTTCTTCTTCTTCTTGTG 129
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 39 AAGCCATGGGGGGAATCTCTAACGCGGTTTCTTCATCCCTCCTCCTGTTGTG 98

QY 130 CACAGAAATTTGTGTACA---GAACCCAGACATGTGAGATTGGCAGATTAATA 186
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 99 CTCAGGAATAGTGTGCAAAAGTAGGAGCAGCAACAGTGTGAACTTCACTACA 158

QY 187 GGGGACATGCTTAA-----GTGTTGTGACACTCACTGACAAACCAAGAGAACGAG 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 159 GGGGACATGCTTCAACACCGGAAGCTGCGACACCACTGCAAGAAAGAGACCTGC 218

QY 241 TTAGGAGAGTGTAGGAGACTTCCGCTGCTGCTGTACTAAAGATTTAAAT 295
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 219 TACAGCGCCCTGCCGACGATTTCCGCTGTTGTGTCACACAGAACTGTTAAAT 273
```

```
RESULT 13
US-10-010-731-11
; Sequence 11, Application US/10010731
; Publication No. US20030041347A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shan, Dilip Maganlal
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
CONTROLLING Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,731
FILING DATE: 13-NO. US20030041347A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/003,198
FILING DATE: 07-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
```


TITLE
JOURNAL
COMMENT

R., Rutter, E., Kohn, S., Shih, T., Jackson, Y., Cardenas, M., McCann
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu

Putative full length read
vector to vector length is This clone is available through: Resgen,
Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801
For further information call: (800)-533-4363 or contact via email:
csh@resgen.com
Seq primer: -40bp from G1bco
High quality sequence stop: 432.

FEATURES
source

Location/Qualifiers
1..487
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1077-1723"
/clone_1lb="Gm-c1077"
/tissue_type="18 day old 'Williams' seedlings"
/dev_stage="18 day old 'Williams' seedlings"
/lab_host="DH10B"
/note="Vector: Bluescript II SK+; Site.1: EcoRI; Site.2:
XhoI. The mRNA was isolated from cotyledons of 18-day-old
'Williams' seedlings which were greenhouse grown in
potting soil. The cotyledons were flash-frozen in liquid
nitrogen. Stratagene's cDNA Synthesis Kit (catalog number
200401) was used to synthesize the cDNA. First-strand
synthesis was performed with 5-methyl dCTP, hence the
ligated cDNA was hemimethylated. A modification of
Stratagene's first-strand synthesis primer was used. An
'anchor' nucleotide (Y-N, C, or G) was added to the 3' end
of the primer (GAGAGAGAGAGAGAGACTGTCGAG(T)18V) to
anchor the primer at the 5' end of the poly(A) tract.
After second-strand synthesis, the cDNA ends were filled
in with cloned Pfu DNA, ligated to EcoRI adapters and
subsequently phosphorylated. The cDNA was then
precipitated and redissolved in sterile, RNase-
free water. The XhoI site within the first-strand
synthesis primer was then restricted by digestion with
XhoI from Promega (40U/ul); all XhoI sites in the cDNA
would be protected by their hemimethylated status. The
cDNA constructs were size-fractionated with a 500bp
cutoff, using Sephacryl S-500 High Resolution (Pharmacia
Biotech) in a 2-mm diameter column and a bed volume of
approximately 1ml. The column eluent was precipitated,
redissolved, and ligated into Stratagene's pBluescript II
XR Predigested vector (pBluescript II SK(+)) vector that
has been digested with EcoRI and XhoI, and phosphorylated
by Stratagene). This library was constructed in the
laboratory of Dr. Paul Keim and Dr. Virginia H. Corryell at
Northern Arizona University."

BASE COUNT 152 a 96 c 102 g 137 t

Query Match 25.7%; Score 125.8; DB 13; Length 487;
Best Local Similarity 68.1%; Pred. No. 8.5e-13;
Matches 224; Conservative 0; Mismatches 92; Indels 13; Gaps 3;

QY 46 TTATATATATTCATCATCATCACTAGTGAAGAAATGAGTGGCTTATGCT 105
DB 39 TTACATACACGTAATCACTAATTAAGCCATGAGAAATCAATAGCTGGTGTGCT 98
QY 106 TCCTCTCTTGGTCTCTCTTGTGACAAAGAAATTTGTGCTG---ACAGAAGCAGAAAT 162
DB 99 TCCTCTCTCTTGTCTCTTGTGCTGCAAGAAATTTGTGCTGCAAGAAATTTGTGCTG 158
QY 163 GTGAGAAATTTGGCAGATAAATATATAGGGGAGCAATGCTT-----TACTGTGTGTGACACTC 216

DB 159 GCGAAGAACTGGGTGATACATACAGGGGTCATGCTTACACACTGCGACATGATGATT 218
QY 217 ACTGCAACACCAAGAAAGACGCACTAGTGAAGGTGTGAGACCACTTCCCTGCTGCT 276
DB 219 TCGCAGAAACCAAGAAAGACGCACTTCTGTCAGAGGAGATGACGAGATTTTCGCTGTTGCT 278
QY 277 GTACTAAAGATGTTAAATGATC---TCCTCCACATCAAGATGTCGATGCAATAGTC 332
DB 279 GCACAAAACACTTTAAATGATCCTTTCATCTCCACATGGAAGATGCAATGCAACGCT 338
QY 333 TTATATATAAATACTAAATATAAATGTC 361
DB 339 ATTTATATAAATAAATACTATATATAC 367

RESULT 6
BG838678/c 426 bp mRNA linear EST 25-MAY-2001
LOCUS BG838678/c
DEFINITION Gc01_03f01_A Gc01_AAFRC_ECORC_cold_stressed_Glycine_clandestina
glycine clandestina cDNA clone Gc01_03f01, mRNA sequence.

ACCESSION BG838678.1 GI:14204985
VERSION BG838678.1 GI:14204985
KEYWORDS EST.
SOURCE Glycine clandestina.
ORGANISM Glycine clandestina
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE 1 (bases 1 to 426)
Singh, J.A., Farah, S., Chapados, J., Couroux, P., De Moors, A., Harris
L.J., Hattori, J.I., Ouellet, T., Robert, L.S., Spott, D. and Tinker
N.A.

TITLE
JOURNAL
COMMENT

Expressed Sequence Tags from cold-stressed Glycine clandestina
Seedlings
Unpublished (2001)
Contact: Singh, J.A.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-Food Canada
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
0C6, Canada
Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@em.agr.ca.

FEATURES
source

Location/Qualifiers
1..426
/organism="Glycine clandestina"
/cultivar="1035"
/db_xref="taxon:45687"
/clone="Gc01_03f01"
/clone_1lb="Gc01_AAFRC_ECORC_cold_stressed_Glycine_clandestina"

/tissue_type="leaves, stem"
/note="Vector: Bluescript SK+/XhoI-EcoRI; Site.1: EcoRI;
Site.2: XhoI; Plants incubated at 2 degrees under 12 hours
of light/day. Harvested after only 2-3 days of cold
treatment. cDNA was prepared with the Uni-Zap cDNA kit
from Stratagene. Eco RI adapters were linked followed by
digest with Xho I/Eco RI and ligated to pBluescript."

BASE COUNT 116 a 92 c 86 g 125 t

Query Match 23.5%; Score 115; DB 12; Length 426;
Best Local Similarity 71.7%; Pred. No. 7e-11; 57; Indels 9; Gaps 2;
Matches 177; Conservative 4; Mismatches 57; Indels 9; Gaps 2;

QY 58 ATCAATCTAATCAATATGAGAAAGAAATCACTAGCTGCTTATGCTTCTCTTCTG 117
DB 420 ATATATATACAGAGCAATGAGAAAGAAATCACTGCTGATTTGCTTCTCTCTG 361
QY 118 TTCTCTTGTGTCACAAAGAAATTTGTGCTG---ACAGAACCCAGAACATGTGAAATTTGG 174

Db 149 ATTCAGGGGTCTATGCATCACCCTCTGCTACCTGGCAGATCAGTGCAGNTCNNNA-CA 207

[illegible][illegible]

OY	334	TTATAAATTAACCTAAATTAATAAATGACAGCCAGTACACTTCACCTCACTCATTAATTA	393
Db	936	MMWMTAATTWTATTATTAAMTWTAATWAATTAATTAATTAATTAATTAATTAATTAATW	995
OY	394	TGACTCAATATCGNGCATACGTATTAGTATGCACCTTCATCATATGGAAATTAACATCA	453
Db	996	WTATATATATATATATTAATAAAMWTAATATTTTMAAAAWTAATATATATATATATW	1055
OY	454	AATAGTATTTTCGTTCACAAAAAATTTTTTTTTT	490
Db	1056	AMWAAATTAATTAATATATATTAAMATRAWMAAAAAMAAM	1092

RESULT_11			
LOCUS	AJ503961	366 bp	mRNA linear EST 09-AUG-2002
DEFINITION	AJ503961 MTAMP Medicago truncatula cDNA clone mtgmadc120040e02, mRNA sequence.		
ACCESSION	AJ503961		
VERSION	AJ503961.1 GI:22084889		
KEYWORDS	EST.		
SOURCE	barrel medic.		
ORGANISM	Medicago truncatula		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosoids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.		
AUTHORS	1 (bases 1 to 366) Menthey,R., Bartelsmeyer,V., Baier,M.C., Meyer,F., Bartels,D., Bekel,T., Linke,B., Grunwald,U., Franken,P., Kuester,H., Perlick,A.M. and Puehler,A. Detection of transcript sequences from mycorrhizal roots of the model mycorrhiza Medicago truncatula genotype A17 - Glomus mosseae using the approach of an EST genome project Unpublished (2002)		
JOURNAL	Contact: Kuester H Lehrstuhl fuer Genetik Universitaet Bielefeld Postfach 100131, D-33501 Bielefeld, Germany.		
COMMENT			
FEATURES	Location/Qualifiers		
source	1..366		
	/organism="Medicago truncatula"		
	/db_xref="taxon:3880"		
	/clone="mtgmadc120040e02"		
	/clone_id="MTAMP"		
	/tissue_type="mycorrhizal roots"		
	/dev_stage="three weeks"		
	/note="vector: pGEM-T; Site_1: PstI; Site_2: SphI; genotype A17; cDNA was prepared from polyA+ enriched RNA from mycorrhizal roots harvested after three weeks. The cDNA was directionally ligated by Medicago into the pGEM-T vector from Promega using GCAATGCCGACGCGCCTATG and CTCACGCCATTAATGGCGGG adapters. Plasmids containing cDNA inserts were propagated in E. coli DH10B cells."		
BASE COUNT	117 a	56 c	76 g 117 t
ORIGIN			
Query Match	10.1%	Score 49.4;	DB 9; Length 366;
Best Local Similarity	68.7%	Pred. No. 21;	
Matches 68;	Conservative 0;	Mismatches 31;	Indels 0; Gaps 0;
OY	48	ATATATATTCATCATCAATCAACAACCTATGGAAGAATACATGCTGCTTATGCTTC	107
Db	23	ATTATTTTAGAACACACAAAAAGAACTGATGGAAGAAACAACTTGCTAGCTTGCTTC	82
OY	108	CCTCTTGCTGCTCTCTTTGTTGTCACACAAAATTTGCTG	146
Db	83	TTTCTCATTTGTTCTCTAGCTGCTCAAGACAGCTGGT	121

RESULT_12	RG453394
-----------	----------

LOCUS	543 bp	MRNA	linear	EST 16-MAR-2001
DEFINITION	BF453394			
ACCESSION	BF453394			
VERSION	BF453394.1			
KEYWORDS	GI:13372188			
SOURCE	EST.			
ORGANISM	barrel medic.			
REFERENCE	Medicago truncatula			
AUTHORS	Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.			
TITLE	1 (bases 1 to 543)			
JOURNAL	Torres-Jerez,I.,Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D.			
COMMENT	Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula leaf library			
FEATURES	Unpublished (2000)			
SOURCE	Contact: May GD			
	Plant Biology Division			
	The Samuel Roberts Noble Foundation			
	2510 Sam Noble Parkway, Ardmore, OK 73402, USA			
	Tel: 580 221 7391			
	Fax: 580 221 7380			
	Email: gdmay@noble.org			
	Insert Length: 543 Std Error: 0.00			
	Plate: 090 row: E column: 11			
	Seq primer: TCACACAGAAACAGCATGAC.			
	Location/Qualifiers			
	1..543			
	/organism="Medicago truncatula"			
	/db_xref="taxon:3880"			
	/clone="NF090E11LF"			
	/clone_11b="Developing leaf"			
	/tissue-type="leaf"			
	/dev-stage="pooled developmental"			
	/note="Vector: lambda zap; Contains a mixture of very young, developing, mature and senescing leaves."			
	110 a 132 c 86 g 210 t 5 others			
BASE COUNT	110 a 132 c 86 g 210 t 5 others			
ORIGIN				
Query Match	10.1%; Score 49.4; DB 12; Length 543;			
Best Local Similarity	66.7%; Pred. No. 17;			
Matches	68; Conservative 0; Mismatches 34; Indels 0; Gaps 0;			
OY	45 TTTATATATATCATCAATCTATATCAAACTATGAGAGAAATCTAGTGGCTTATGC 104			
DB	363 TTTCTTTCTTTANNAACAAACAAAAGAACTGATGAGANNAAGAAACACTGTGATGCTTGTC 422			
OY	105 TTCCCTCTTGGCTGCTCTGCTGTCGACAAAGAAATGGGCG 146			
DB	423 TTCTTCTCATTTGTTCTTGTAGCTGCTCAANNAAGAGTGGTG 464			
RESULT 13				
LOCUS	BF452703			
DEFINITION	BF452703			
ACCESSION	BF452703			
VERSION	BF452703.1			
KEYWORDS	GI:13371497			
SOURCE	EST.			
ORGANISM	barrel medic.			
	Medicago truncatula			
	Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.			
	1 (bases 1 to 452)			
	Torres-Jerez,I.,Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D.			
	Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula leaf library			
TITLE				

JOURNAL
COMMENT Unpublished (2000)
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 452 Std Error: 0.00
Plate: 079 row: E column: 01
Seq primer: TCACACGGAACGCTATGAC.
Location/Qualifiers
1. .452
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF079E01LF"
/clone_1lb="Developing leaf"
/tissue_type="leaf"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of very young, developing, mature and senescing leaves."

BASE COUNT 158 a 60 c 89 g 145 t
ORIGIN

Query Match 10.0%; Score 49.2; DB 12; Length 452;
Best Local Similarity 70.2%; Pred. No. 21;
Matches 66; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

OY 53 TATTCATCATCTAATCAATGAGAGAAATGCTGCTT 112
| | | | | | | | | | | | | | | | | | | | | |
Db 3 TTTCAGACACAAAAGAGATGAGAGAAAACACTTCTGCTTCTTCT 62
| | | | | | | | | | | | | | | | | | | | | |
OY 113 CTGTGCTCTTGTGACAGAAATGTGCTG 146
| | | | | | | | | | | | | | | | | | | | | |
Db 63 CATGTCTCTTAGCTGCTCAAGACAGTGTG 96
| | | | | | | | | | | | | | | | | | | | | |

RESULT 14
LOCUS B0157500 466 bp mRNA linear EST 24-APR-2002
DEFINITION NF105E08IR1067 Irradiated Medicago truncatula cDNA clone
ACCESSION B0157500
VERSION B0157500.1 GI:20294559
KEYWORDS EST.
SOURCE barbel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 466)
Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula Irradiated library
Unpublished (2001)
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 466 Std Error: 0.00
Plate: 105 row: E column: 08
Seq primer: TCACACGGAACGCTATGAC.
Location/Qualifiers
1. .466
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF105E08IR"
/clone_1lb="Irradiated"

FEATURES
source

/tissue_type="seedlings"
/dev_stage="seedling"
/note="Vector: Lambda Zap; Seedlings were exposed either to 100 Gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation. Gamma-irradiated samples were harvested at 6, 12, 24 and 48 hours after treatment. UV-irradiated samples were harvested 24 hours post-treatment. cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from each sample. The cDNA was directionally ligated into the uni-zap XR vector (Stratagene) and packaged using the Gigapack III gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant uni-zap XR vector using ExAssist helper phage and the E. coli strain XL1-blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."

BASE COUNT 162 a 64 c 94 g 146 t
ORIGIN

Query Match 10.0%; Score 49.2; DB 14; Length 466;
Best Local Similarity 70.2%; Pred. No. 20;
Matches 66; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

OY 53 TATTCATCATCTAATCAATGAGAGAAATGCTGCTT 112
| | | | | | | | | | | | | | | | | | | | | |
Db 10 TTTCAGACACAAAAGAGATGAGAGAAAACACTTCTGCTTCTTCT 69
| | | | | | | | | | | | | | | | | | | | | |
OY 113 CTGTGCTCTTGTGACAGAAATGTGCTG 146
| | | | | | | | | | | | | | | | | | | | | |
Db 70 CATGTCTCTTAGCTGCTCAAGACAGTGTG 103
| | | | | | | | | | | | | | | | | | | | | |

RESULT 15
LOCUS B1269947 447 bp mRNA linear EST 18-JUL-2001
DEFINITION NF017612IR1099 Irradiated Medicago truncatula cDNA clone
ACCESSION B1269947
VERSION B1269947.1 GI:14877082
KEYWORDS EST.
SOURCE barbel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 447)
Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula Irradiated library
Unpublished (2001)
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 447 Std Error: 0.00
Plate: 017 row: G column: 12
Seq primer: TCACACGGAACGCTATGAC.
Location/Qualifiers
1. .447
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF017612IR"
/clone_1lb="Irradiated"
/tissue_type="seedlings"
/dev_stage="seedling"
/note="Vector: Lambda Zap; Seedlings were exposed either to 100 Gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation. Gamma-irradiated samples were harvested at 6, 12, 24 and

FEATURES
source

THIS PAGE BLANK (USPTO)

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2003, 05:17:37 ; Search time 572.217 Seconds

(without alignments)
7018.649 Million cell updates/sec

Title: US-10-010-731-13_COPY_105_242

Perfect score: 138
Sequence: 1 AGACATGAGAGATTGGC.....GGTGTACTAAAGATGTAA 138Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

```
GenBml:
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_ph:*
7: gb_pl:*
8: gb_pl:*
9: gb_dr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_cm:*
21: em_ov:*
22: em_ph:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_in:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	138	100.0	406	8	AF319468	AF319468 Medicago
2	88.6	64.2	363	8	AF139018	AF139018 Pisum sat
3	88.6	64.2	468	8	PEADRR230A	LO1578 Pea (P1230)
4	88.6	64.2	468	8	PSP1230	X52225 P.sativum p
5	61.4	44.5	494	6	AX252303	AX252303 Sequence
6	58.2	42.2	496	8	AB020613	AB020613 Vigna rad
7	55	35.7	459	8	VUSTORED	X16877 Vigna unguil
8	49.2	39.9	380	8	AB049718	AB049718 Pisum sat
9	40	29.0	141	6	A27063	A27063 L.cleera Af
10	40	29.0	141	6	AR050147	AR050147 Sequence
11	40	29.0	141	6	AR130266	AR130266 Sequence
12	40	29.0	141	6	AR130266	AR130266 Sequence
13	40	29.0	141	6	AR130266	AR130266 Sequence
14	39.6	28.7	456	8	PEADRR230B	X52224 P.sativum p
15	39.6	28.7	456	8	PSP139	AC127931 Rattus no
16	34.2	24.8	160480	2	AC105077	AC105077 Mus muscu
17	32.8	23.8	208342	2	AC105077	AC105077 Mus muscu
18	32.4	23.5	110626	9	AC005541	AC005541 Homo sapi
19	32.4	23.5	110626	9	AC005541	AC005541 Homo sapi
20	32.4	23.5	110626	9	AC005541	AC005541 Homo sapi
21	31.8	23.0	161390	9	AC013414	AC013414 Homo sapi
22	31.8	23.0	161390	9	AC013414	AC013414 Homo sapi
23	31.6	22.9	133843	8	AC003981	AC003981 Genomic s
24	31.2	22.6	83276	2	AC026631	AC026631 Homo sapi
25	31.2	22.6	167293	2	AC022629	AC022629 Homo sapi
26	31.2	22.6	167293	2	AC022629	AC022629 Homo sapi
27	30.8	22.3	25560	9	AP000298	AP000298 Homo sapi
28	30.8	22.3	40791	9	AF039907	AF039907 Homo sapi
29	30.8	22.3	100000	9	AP000044	AP000044 Homo sapi
30	30.8	22.3	100000	9	AP000112	AP000112 Homo sapi
31	30.8	22.3	100000	9	AP000188	AP000188 Homo sapi
32	30.8	22.3	141689	2	AC128028	AC128028 Rattus no
33	30.8	22.3	186661	2	AC125570	AC125570 Rattus no
34	30.8	22.3	340000	9	AP001716	AP001716 Homo sapi
35	30.6	22.2	141276	9	AC096478	AC096478 Rattus no
36	30.6	22.2	168319	2	AC023282	AC023282 Homo sapi
37	30.6	22.2	171799	2	AC098593	AC098593 Mus muscu
38	30.6	22.2	187607	2	AC102122	AC102122 Mus muscu
39	30.6	22.2	198607	2	AC130721	AC130721 Mus muscu
40	30.6	22.2	347162	10	AC084070	AC084070 Mus muscu
41	30.4	22.0	1740	9	AB047901	AB047901 Macaca fa
42	30.4	22.0	37948	6	AR166758	AR166758 Sequence
43	30.4	22.0	99042	2	AC123238	AC123238 Rattus no
44	30.4	22.0	162973	2	AC016307	AC016307 Homo sapi
45	30.4	22.0	163621	9	AC112129	AC112129 Homo sapi

ALIGNMENTS

```
RESULT 1
AF319468
LOCUS
DEFINITION Medicago sativa antifungal protein precursor, mRNA, complete cds.
ACCESSION AF319468
VERSION AF319468.1 GI:11762085
KEYWORDS
SOURCE
ORGANISM Medicago sativa.
Medicago sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
REFERENCE
1 (bases 1 to 406)
Liang,J., Shah,D.M., Wu,Y.S., Rosenberger,C.A. and Hakimi,S.
```

TITLE Antifungal Polypeptide(s) and Methods for Controlling Plant Pathogenic Fungi
JOURNAL Patent: US 6121436 19-SEP-2000;
REFERENCE Monsanto Company; St Louis, MO
AUTHORS 2 (bases 1 to 406)
TITLE Gao, A.G., Hakimi, S.M., Mittanck, C.A., Wu, Y., Woerner, B.M., Stark, D.M., Shah, D.M., Liang, J., and Rommens, C.M.
JOURNAL Fungal pathogen protection in potato by expression of a plant defensin peptide
MEDLINE Nat. Biotechnol. 18 (12), 1307-1310 (2000)
PUBMED 2053844
11101813
REFERENCE 3 (bases 1 to 406)
AUTHORS Mittanck, C.A., Wu, Y., Hakimi, S.M., Liang, J., Shah, D.M. and Gao, A.G.
TITLE Direct Submission
JOURNAL Submitted (04-NOV-2000) Monsanto Company, 700 Chesterfield Parkway, St Louis, MO 63198, USA

FEATURES
source
1..406
/organism="Medicago sativa"
/db_xref="taxon:3879"
75..293
/note="alfAFP: defensin"
/codon_start=1
/product="antifungal protein precursor"
/protein_id="AAG40321.1"
/db_xref="GI:11762086"
/translation="MERKSLAGCFELVLFVAQELIVTEARTCENTLADKYKPCPSG
CDHCTKENVASGRCDRDFRCWCKRNC"
75..155
sig_peptide
156..290
mat_peptide
/product="antifungal protein"
BASE COUNT 140 a 74 c 78 g 114 t
ORIGIN

Query Match 100.0%; Score 138; DB 8; Length 406;
Best local Similarity 100.0%; Pred. No. 3.9e-33;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGACATGTGAGATTGGCAGATAATATAGGGACCATCTTTAGTGTGTGACACT 60
|||||
DB 156 AGAACATGTGAGATTGGCAGATAATATAGGGACCATCTTTAGTGTGTGACACT 215
|||||

QY 61 CACTGCACAACCAAGAGAACGAGTTAGTGAAGGTGAGGACGACTCCGCTGCTGG 120
|||||
DB 216 CACTGCACAACCAAGAGAACGAGTTAGTGAAGGTGAGGACGACTCCGCTGCTGG 275
|||||

QY 121 TGTACTAAAGATGTAA 138
|||||
DB 276 TGTACTAAAGATGTAA 293
|||||

RESULT 2
AF139018 363 bp mRNA linear PLN 02-JAN-2001
LOCUS P139018
DEFINITION Pisum sativum disease resistance response protein 230 precursor
(DNR230) mRNA, complete cds.
ACCESSION AF139018
VERSION AF139018.1 GI:12002298
KEYWORDS
SOURCE Pisum sativum.
ORGANISM Pisum sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
REFERENCE 1 (bases 1 to 363)
AUTHORS Savenstrand, H., Brosche, M. and Strid, A.
TITLE Pisum sativum cv. Greentest
JOURNAL unpublished
REFERENCE 2 (bases 1 to 363)
AUTHORS Savenstrand, H., Brosche, M. and Strid, A.

TITLE Direct Submission
JOURNAL Submitted (29-MAR-1999) Biochemistry and Biophysics, Goteborg University, Medicinaregatan 9c, P.O. Box 462, Goteborg S-40530, Sweden

FEATURES
source
Location/Qualifiers
1..363
/organism="Pisum sativum"
/cultivar="Greenfeast"
/db_xref="taxon:3888"
1..363
gene
/gene="DNR230"
56..274
CDS
/gene="DNR230"
/note="Ozone-induced; similar to the Pisum sativum cv. Alaska product encoded by GenBank Accession Number L01578"
/codon_start=1
/product="disease resistance response protein 230 precursor"
/protein_id="AAG43285.1"
/db_xref="GI:12002299"
/translation="MERKSLAGCFELVLFVAQELIVSEANTCENTLADKYKVCFCG
CDHCTOBGALSGCRDPRFCWCKRNC"
BASE COUNT 113 a 68 c 74 g 108 t
ORIGIN

Query Match 64.2%; Score 88.6; DB 8; Length 363;
Best local Similarity 78.5%; Pred. No. 1.9e-17;
Matches 106; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 4 ACATGTGAGATTGGCAGATAATATAGGGACCATCTTTAGTGTGTGACACTAC 63
|||||
DB 140 ACATGTGAGATTGGCAGATAATATAGGGACCATCTTTAGTGTGTGACACTAC 199
|||||

QY 64 TGCACAACCAAGAGAACGAGTTAGTGAAGGTGAGGACGACTCCGCTGCTGG 123
|||||
DB 200 TGTAGACACACAGAGGCCGCAATTACGCGACATGACGAGATGATCTTGGCTTGGTGC 259
|||||

QY 124 ACTAAAGATGTAA 138
|||||
DB 260 ACTAAAGATGTAA 274
|||||

RESULT 3
PEADRR230A 468 bp mRNA linear PLN 11-FEB-2002
LOCUS PEA230A
DEFINITION Pea (P1230) disease resistance response protein 230 (DNR230-a) mRNA, complete cds.
ACCESSION L01578.1 GI:169073
VERSION L01578.1
KEYWORDS cysteine-rich protein; disease resistance response protein 230; pathogenesis-related protein.
SOURCE Pisum sativum.
ORGANISM Pisum sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
REFERENCE 1 (bases 1 to 468)
AUTHORS Chiang, C.C. and Hadwiger, L.A.
TITLE The Fusarium solani-induced expression of a pea gene family encoding high cysteine content proteins
JOURNAL Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)
MEDLINE 9210628
PUBMED 1799696
COMMENT On Feb 8, 2002 this sequence version replaced gi:247416.
FEATURES
source
Location/Qualifiers
1..468
/organism="Pisum sativum"
/strain="Alaska"
/db_xref="taxon:3888"
/tissue_type="pod tissue treated with Fusarium solani conidia"
/dev_stage="immature"

gene
1..468
/gene="DRR230-a"
78..296
/codon_start=1
/protein_id="CAA36474.1"
/db_xref="GI:22208749"
/translation="MEKSLACLSFLLVLFVAQEIIVSEANTCENLAGSYKGVCFGG
CDRHCRTQEGAIISGRCDRDFRCWCTKNC"
159..293
/gene="PI230"
/product="unnamed"
/product="PI230"
/protein_id="AAA9117.1"
/db_xref="GI:169074"
/translation="MEKSLACLSFLLVLFVAQEIIVSEANTCENLAGSYKGVCFGG
CDRHCRTQEGAIISGRCDRDFRCWCTKNC"
159..293
mat_peptide
/gene="DRR230-a"
/product="disease resistance response protein"
/function="unknown"
/note="determined by in vitro cleavage with microsomal
membranes"
/evidence="experimental"
BASE COUNT 153 a 88 c 84 g 143 t
ORIGIN
Query Match 64.2%; Score 88.6; DB 8; Length 468;
Best Local Similarity 78.5%; Pred. No. 1.8e-17;
Matches 106; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 4 ACATGTGAGAAATTTGGCAGATAATATATAGGGAGCCATGCTTATGTTGTCACACTC 63
|||||
DB 162 ACATGTGAGAAATTTGGCTGTCATATAGGAGATGCTTGGTGATGTACCGCTC 221
|||||
QY 64 TGCACACCAAGAACAGCAGTGTAGTGAAGTGTAGGAGACACTTCGCTGCTGCTGT 123
|||||
DB 222 TGTAGACACACAGAGGCGCAATTTAGCGGACAGATGACGATCTTCTGTTGCTGC 281
|||||
QY 124 ACTAAAGATGTTAA 138
|||||
DB 282 ACTAAAGATGTTAA 296
|||||
RESULT 4
PSP1230 468 bp mRNA linear PLN 09-AUG-2002
LOCUS P.sativum p1230 mRNA.
DEFINITION X52225
ACCESSION X52225.1 GI:22208748
VERSION X52225.1
KEYWORDS secreted protein.
SOURCE pea.
ORGANISM Pisum sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;
Pisum.
REFERENCE
AUTHORS Chiang,C.C. and Hadwiger,L.A.
TITLE The fusarium solani-induced expression of a pea gene family
encoding high cysteine content proteins
JOURNAL Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)
MEDLINE 92190628
REFERENCE 2 (bases 1 to 468)
AUTHORS Chiang,C.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1990) Chiang C., Washington State University,
Dept. of Plant Pathology, Pullman, WA 99164-6430, USA
FEATURES
source
1..468
/organism="Pisum sativum"
/db_xref="taxon:3888"
/tissue_type="endocarp"
1..468
/gene="PI230"
78..296
CDS

sig_peptide
/gene="PI230"
/codon_start=1
/protein_id="CAA36474.1"
/db_xref="GI:22208749"
/translation="MEKSLACLSFLLVLFVAQEIIVSEANTCENLAGSYKGVCFGG
CDRHCRTQEGAIISGRCDRDFRCWCTKNC"
78..158
/gene="PI230"
159..293
mat_peptide
/gene="PI230"
/product="unnamed"
BASE COUNT 153 a 88 c 84 g 143 t
ORIGIN
Query Match 64.2%; Score 88.6; DB 8; Length 468;
Best Local Similarity 78.5%; Pred. No. 1.8e-17;
Matches 106; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 4 ACATGTGAGAAATTTGGCAGATAATATATAGGGAGCCATGCTTATGTTGTCACACTC 63
|||||
DB 162 ACATGTGAGAAATTTGGCTGTCATATAGGAGATGCTTGGTGATGTACCGCTC 221
|||||
QY 64 TGCACACCAAGAACAGCAGTGTAGTGAAGTGTAGGAGACACTTCGCTGCTGCTGT 123
|||||
DB 222 TGTAGACACACAGAGGCGCAATTTAGCGGACAGATGACGATCTTCTGTTGCTGC 281
|||||
QY 124 ACTAAAGATGTTAA 138
|||||
DB 282 ACTAAAGATGTTAA 296
|||||
RESULT 5
AX252303 494 bp DNA linear PAT 05-OCT-2001
LOCUS Sequence 5 from Patent WO0168887.
DEFINITION AX252303
ACCESSION AX252303
VERSION AX252303.1 GI:15985643
KEYWORDS
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE
1 (bases 1 to 494)
AUTHORS Jung,R. and Kinney,A.J.
TITLE Hypoallergenic transgenic soybeans
JOURNAL Patent: WO 0168887-A 5 20-SEP-2001;
E. I. du Pont de Nemours and Company (US); PIONEER HI-BRED
INTERNATIONAL, INC. (US)
FEATURES
source
1..494
/organism="Glycine max"
/db_xref="taxon:3847"
BASE COUNT 153 a 97 c 103 g 134 t 7 others
ORIGIN
Query Match 44.5%; Score 61.4; DB 6; Length 494;
Best Local Similarity 70.2%; Pred. No. 7.8e-09;
Matches 99; Conservative 0; Mismatches 36; Indels 6; Gaps 1;
QY 4 ACATGTGAGAAATTTGGCAGATAATATATAGGGAGCCATGCTT-----TGTGTTGTGAC 57
|||||
DB 133 ACTGTGAGAACTTGGCTGTATATACAGGGGCTCATGCTTACCACTGCGACGTCGAT 192
|||||
QY 58 ACTCACTGCACACCAAGAGAGCAGTGTAGTGAAGTGTAGGAGACACTTCGCTGC 117
|||||
DB 193 GATCACTGCACACCAAGAGAGCAGTGTGTGAGAGAGATGACGAGGACATTTTGCCT 252
|||||
QY 118 TGTGTACTTAAAGATGTTAA 138
|||||
DB 253 TGTGTACCAACCAAAACTGTTAA 273
|||||

```

RESULT 6
AB020613
LOCUS AB020613 496 bp mRNA linear PLN 05-JAN-2002
DEFINITION Vigna radiata mRNA for PDF1, complete cds.
ACCESSION AB020613
VERSION AB020613.1 GI:18146787
KEYWORDS PDF1.
SOURCE Vigna radiata (strain:B20F5 9-3-2-2) immature seed cDNA to mRNA, clone lib:B20 clone:PDF-1.
ORGANISM Vigna radiata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.

REFERENCE
1 Ishimoto, M. and Kaga, A.
AUTHORS Munbean defensin
TITLE Published Only in Database (2002)
JOURNAL 2 (bases 1 to 496)
REFERENCE 2 (bases 1 to 496)
AUTHORS Ishimoto, M. and Kaga, A.
TITLE Direct Submission
JOURNAL Submitted (01-DEC-1998) Masao Ishimoto, Chugoku National Agricultural Experiment Station, Laboratory of Plant Biotechnology; 6-12-1 Nishitokatsu, Fukuyama, Hiroshima 721-8514, Japan (E-mail:ishimoto@cgk.affrc.go.jp, Tel:+81-849-234100(ex.231), Fax:+81-849-247893)

FEATURES
source
1..496
location/Qualifiers
/organism="Vigna radiata"
/strain="B20F5 9-3-2-2"
/db_xref="taxon:157791"
/clone="PDF-1"
/tissue_type="immature seed"
/clone_lib="B20"
1..496
/gene="PDF1"
/gene="PDF1"
46..273
/gene="PDF1"
/codon_start=1
/product="PDF1"
/protein_id="BAB82453.1"
/db_xref="GI:18146787"
/translation="MEKSLAGLCFLVLFVYAEVMOVTEAKTCENTLVYRGPCTT
TGSCDHCKNKKEHLISGRCDRCWCTRNC"
496
polyA_site
/gene="PDF1"
/note="17 a nucleotides"
BASE COUNT 148 a 104 c 106 g 138 t
ORIGIN
Query Match 42.2%; Score 58.2; DB 8; Length 496;
Best Local Similarity 68.8%; Pred. No. 8.1e-08;
Matches 97; Conservative 0; Mismatches 38; Indels 6; Gaps 1;

QY 4 ACATGTGAGATTGGCAGATAATATAGGGACCATGCTT-----TAGTGGTGTGAC 57
DB 133 ACTTGGAGAACCTGGCGAATACCTGACAGGGGTCATGCTTACCACTGGCAGCTGCAT 192
QY 58 ACTCACTGCACCAAGCAAGACGAGTGTAGTGAAGGTGAGGACGACTCCGCTGC 117
DB 193 GATCACTGCAGAACCAAGAACACTGAGAGTGAGTGAGGAGGACGATTTCCGGGTG 252
QY 118 TGCTGTACTTAAAGATGTTAA 138
DB 253 TGCTGCACTAAGAACTGTAA 273

```

```

VERSION X16877.1 GI:22075
KEYWORDS
SOURCE Vigna radiata.
ORGANISM Vigna radiata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.

REFERENCE
1 (bases 1 to 459)
AUTHORS Yamauchi, D.
TITLE Direct Submission
JOURNAL Submitted (10-OCT-1989) Yamauchi D., Dept of Biology, Tokyo Metropolitan University, Fuchazawa 2-1, Setagaya-ku, Tokyo 158, Japan
2 (bases 1 to 459)
AUTHORS Ishibashi, N., Yamauchi, D. and Minamikawa, T.
TITLE Stored mRNA in cotyledons of Vigna unguiculata seeds: nucleotide sequence of cloned cDNA for a stored mRNA and induction of its synthesis by precocious germination
JOURNAL Plant Mol. Biol. 15 (1), 59-64 (1990)
MEDLINE 91355865
PUBMED 2103443

FEATURES
source
1..459
location/Qualifiers
/organism="Vigna radiata"
/db_xref="taxon:157791"
/clone="PSAS10"
/tissue_type="cotyledon"
/clone_lib="lambda gtl10"
/dev_stage="seed"
14..241
/note="PSAS10 ORF"
/codon_start=1
/protein_id="CAA34760.1"
/db_xref="GI:22076"
/db_xref="SWISS-PROT:P18646"
/translation="MEKSLAGLCFLVLFVYAEVMOVTEAKTCENTLVYRGPCTT
TGSCDHCKNKKEHLISGRCDRCWCTRNC"
136 a 91 c 99 g 133 t
ORIGIN
Query Match 39.9%; Score 55; DB 8; Length 459;
Best Local Similarity 67.4%; Pred. No. 8.4e-07;
Matches 95; Conservative 0; Mismatches 40; Indels 6; Gaps 1;

QY 4 ACATGTGAGATTGGCAGATAATATAGGGACCATGCTT-----TAGTGGTGTGAC 57
DB 101 ACTTGGAGAACCTGGCGAATACCTGACAGGGGTCATGCTTACCACTGGCAGCTGCAT 160
QY 58 ACTCACTGCACCAAGCAAGACGAGTGTAGTGAAGGTGAGGACGACTCCGCTGC 117
DB 161 GATCACTGCAGAACCAAGAACACTGCTGAGTGAGTGAGGAGGATGATGCCGGTGT 220
QY 118 TGCTGTACTTAAAGATGTTAA 138
DB 221 TGCTGCACTAAGAACTGTAA 241

RESULT 8
AB049718/c
LOCUS AB049718 380 bp mRNA linear PLN 08-JUN-2001
DEFINITION Pisum sativum ssa-8 mRNA for putative senescence-associated protein, complete cds.
ACCESSION AB049718
VERSION AB049718.1 GI:13359440
KEYWORDS
SOURCE Pisum sativum (cultivar:Ichihara wase) immature pods cDNA to mRNA.
ORGANISM Pisum sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.

```

REFERENCE 1 (sites)
AUTHORS Parlasca,J.A.T., Sunaga,A., Miyazaki,T., Hisaka,H., Sonoda,M.,
TITLE Nakagawa,H. and Sato,T.
JOURNAL Cloning of cDNAs encoding senescence-associated genes, ACC synthase
and ACC oxidase from stored snow pea pods (Pisum sativum L. var
saccharatum) and their expression during pod storage
Postharvest Biology and Technology 22, 239-247 (2001)
REFERENCE 2 (bases 1 to 380)
AUTHORS Parlasca,J.A. and Sato,T.
TITLE Direct Submission
JOURNAL Submitted (06-OCT-2000) Takahide Sato, Chiba University, Faculty of
Horticulture, 648 Matsudo, Matsudo, Chiba 271-8510, Japan
(E-mail:satoemidori.h.chiba-u.ac.jp, Tel:81-47-308-8863)
FEATURES
SOURCE Location/Qualifiers
1..380
/organism="Pisum sativum"
/cultivar="Ichihara wase"
/db_xref="taxon:3888"
/tissue_type="pods"
/dev_stage="immatured pods"
/country="Japan: Chiba, Matsudo"
/note="CDNs isolated from a 5-day stored pod cDNA library
by differential screening".
1..380
/gene="ssa-8"
98..370
/gene="ssa-8"
/codon_start=1
/product="putative senescence-associated protein"
/protein_id="BAB3416.1"
/db_xref="GI:13359441"
/translation="MHDIETHNSGRIOHNGAVOILIIYFIHIMSFIHLILSLR
VGENMINFECTSSNHPCSTSHVCARSCNVCCSYHLGCMVPRY"
BASE COUNT 120 a 78.c 64 g 118 t
ORIGIN
Query Match 35.7%; Score 49.2; DB 8; Length 380;
Best Local Similarity 70.2%; Pred. No. 5.8e-05;
Matches 66; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 45 TAGGTGGTGTGACACTGACACTGACACCAAGAAAGCAAGTGTAGTAGGGA 104
DB 339 TGGTAACGCAACAAACATTGCGAGAACAGCACATGAGTGGAGGTGACGGA 280
QY 105 CGACTCCGCTGCTGTCTACTTAAAGATGTTAA 138
DB 279 TGAATTTTCGCTGCTGCTGCACTGCAAACTGTTAA 246
RESULT 9
LOCUS A27063 141 bp DNA linear PAT 12-JUN-1995
DEFINITION L.cicera AFP sequence.
ACCESSION A27063
VERSION A27063.1 GI:1247357
KEYWORDS
SOURCE Lathyrus cicera.
ORGANISM Lathyrus cicera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;
Lathyrus.
FEATURES
SOURCE Location/Qualifiers
1..141
/organism="Lathyrus cicera"
/db_xref="taxon:3856"
BASE COUNT 43 a 30 c 32 g 33 t 3 others
ORIGIN
Query Match 29.0%; Score 40; DB 6; Length 141;
Best Local Similarity 60.6%; Pred. No. 0.049;
Matches 83; Conservative 0; Mismatches 48; Indels 6; Gaps 1;

QY 4 ACATGAGAAATTTGGCAGATAAATATAGGGACCATGCTTAGTGT-----TGTGAC 57
DB 4 ACTTGGAGAACCTTCTTGAACTTCAGAGGACATGATTCACATGGAACCTGCAC 63
QY 58 ACTCACTGCACACCAAGAGAACGAGTTAGTGAAGGTGTAGGACGACTTCGCTGC 117
DB 64 AAGCATTTGCAAGAACAGACAGATCTTCTTGTGAAAGATGACAGATATTTCCNNTGC 123
QY 118 TGGTGTACTTAAAGATG 134
DB 124 TGGTGCCTAGAAACTG 140
RESULT 10
LOCUS A39547 141 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 35 from Patent WO9416076.
ACCESSION A39547
VERSION A39547.1 GI:2295840
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 141)
AUTHORS Dubock,A.C., Powell,K.A. and Rees,S.B.
TITLE ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
JOURNAL Patent: WO 9416076-A 35 21-JUL-1994;
ZENECA LTD (GB)
COMMENT Other publication AU 5820494 940815.
FEATURES
SOURCE Location/Qualifiers
1..141
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 43 a 30 c 32 g 33 t 3 others
ORIGIN
Query Match 29.0%; Score 40; DB 6; Length 141;
Best Local Similarity 60.6%; Pred. No. 0.049;
Matches 83; Conservative 0; Mismatches 48; Indels 6; Gaps 1;
QY 4 ACATGTGAGAAATTTGGCAGATAAATATAGGGACCATGCTTAGTGT-----TGTGAC 57
DB 4 ACTTGGAGAACCTTCTTGAACTTCAGAGGACATGATTCACATGGAACCTGCAC 63
QY 58 ACTCACTGCACACCAAGAGAACGAGTTAGTGAAGGTGTAGGACGACTTCGCTGC 117
DB 64 AAGCATTTGCAAGAACAGACAGATCTTCTTGTGAAAGATGACAGATATTTCCNNTGC 123
QY 118 TGGTGTACTTAAAGATG 134
DB 124 TGGTGCCTAGAAACTG 140
RESULT 11
LOCUS AR050147 141 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 35 from patent US 5824869.
ACCESSION AR050147
VERSION AR050147.1 GI:5972139
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 141)
AUTHORS Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
Tjerraa,F.R.G. and Vanderleyden,J.
TITLE Bioticidal proteins
JOURNAL Patent: US 5824869-A 35 20-OCT-1998;
FEATURES
SOURCE Location/Qualifiers
1..141
/organism="unknown"
BASE COUNT 43 a 30 c 32 g 33 t 3 others
ORIGIN

Query Match 29.0%; Score 40; DB 6; Length 141;
Best Local Similarity 60.6%; Pred. No. 0.049;
Matches 83; Conservative 0; Mismatches 48; Indels 6; Gaps 1;

LOCUS ARI30266 141 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 35 from patent US 6187904.
ACCESSION ARI30266
VERSION ARI30266.1 GI:14118163
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 141)
AUTHORS Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
Terras, F.R.G. and Vanderleyden, J.
TITLE Biochemical proteins
JOURNAL Patent: US 6187904-A 35 13-FEB-2001;
FEATURES
Source Location/Qualifiers
1..141
/organism="unknown"

BASE COUNT 43 a 30 c 32 g 33 t 3 others

Query Match 29.0%; Score 40; DB 6; Length 141;
Best Local Similarity 60.6%; Pred. No. 0.049;
Matches 83; Conservative 0; Mismatches 48; Indels 6; Gaps 1;

LOCUS ARI30266 141 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 35 from patent US 6187904.
ACCESSION ARI30266
VERSION ARI30266.1 GI:14118163
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 141)
AUTHORS Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
Terras, F.R.G. and Vanderleyden, J.
TITLE Biochemical proteins
JOURNAL Patent: US 6187904-A 35 13-FEB-2001;
FEATURES
Source Location/Qualifiers
1..141
/organism="unknown"

BASE COUNT 43 a 30 c 32 g 33 t 3 others

Query Match 29.0%; Score 40; DB 6; Length 141;
Best Local Similarity 60.6%; Pred. No. 0.049;
Matches 83; Conservative 0; Mismatches 48; Indels 6; Gaps 1;

LOCUS ARI30266 141 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 35 from patent US 6187904.
ACCESSION ARI30266
VERSION ARI30266.1 GI:14118163
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 141)
AUTHORS Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
Terras, F.R.G. and Vanderleyden, J.
TITLE Biochemical proteins
JOURNAL Patent: US 6187904-A 35 13-FEB-2001;
FEATURES
Source Location/Qualifiers
1..141
/organism="unknown"

BASE COUNT 43 a 30 c 32 g 33 t 3 others

Query Match 29.0%; Score 40; DB 6; Length 141;
Best Local Similarity 60.6%; Pred. No. 0.049;
Matches 83; Conservative 0; Mismatches 48; Indels 6; Gaps 1;

LOCUS ARI30266 141 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 35 from patent US 6187904.
ACCESSION ARI30266
VERSION ARI30266.1 GI:14118163
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 141)
AUTHORS Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
Terras, F.R.G. and Vanderleyden, J.
TITLE Biochemical proteins
JOURNAL Patent: US 6187904-A 35 13-FEB-2001;
FEATURES
Source Location/Qualifiers
1..141
/organism="unknown"

BASE COUNT 43 a 30 c 32 g 33 t 3 others

BASE COUNT 43 a 30 c 32 g 33 t 3 others

Query Match 29.0%; Score 40; DB 6; Length 141;
Best Local Similarity 60.6%; Pred. No. 0.049;
Matches 83; Conservative 0; Mismatches 48; Indels 6; Gaps 1;

LOCUS PEADR230B 456 bp mRNA linear PLN 11-FEB-2002
DEFINITION Pisum sativum disease resistance response protein 39 (DDR230-b)
ACCESSION L01579.1 GI:169075
VERSION L01579.1 GI:169075
KEYWORDS cysteine-rich protein; disease resistance response protein 39;
pathogenesis-related protein.
SOURCE Pisum sativum (strain Alaska) cDNA to mRNA.
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;
Pisum.
REFERENCE 1 (bases 1 to 456)
AUTHORS Chhang, C.C. and Hadwiger, L.A.
TITLE The Fusarium solani-induced expression of a pea gene family
encoding high cysteine content proteins
JOURNAL Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)
MEDLINE 92190628
PUBMED 1799696
COMMENT On Feb 8, 2002 this sequence version replaced gi:247414.
FEATURES
Source Location/Qualifiers
1..456
/organism="Pisum sativum"
/strain="Alaska"
/db_xref="taxon:3888"
/tissue_type="pod tissue treated with Fusarium solani
conidia."
/dev_stage="immature"
1..456
/gene="DDR230-b"
69..293
/gene="DDR230-b"
/function="unknown"
/standard_name="pathogenesis related protein"
/evidence="experimental"
/product="disease resistance response protein 39"
/protein_id="AAI9118.1"
/db_xref="GI:169076"
/translation="MEKSLALSPILLIVFAQEIIVTEANTCEHLADTVRGVCFET
NASCDHCKKAKHLISGTCHDMKCFCTQNC"
153..290
/gene="DDR230-b"
/product="disease resistance response protein"
/function="unknown"
/standard_name="pathogenesis related protein"
/note="citolcleavage determined by homology with p1230;
putative"

BASE COUNT 155 a 81 c 79 g 141 t

THIS PAGE BLANK (USPTO)

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2003, 03:16:57 ; Search time 76.9108 Seconds
(without alignments)
4040.728 Million cell updates/sec

Title: US-10-010-731-13_COPY_105_242
Perfect score: 138
Sequence: 1 AGAAGATGTGAGAAATTTGCG.....GGTGTACTAAAGATGTTAA 138

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
N.Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	138	100.0	250	19	AAV39187
2	138	100.0	490	19	AAV39186
3	138	100.0	507	19	AAV39195
4	119.4	86.5	200	19	AAV39190
5	117.8	85.4	327	19	AAV39194
6	88.6	64.2	468	21	AAZ49412
7	86.6	62.8	293	19	AAV39191
8	61.4	44.5	494	22	AAAD17530
9	40	29.0	141	15	AAO70126

c	10	39	28.3	47	19	AAV39197	Antifungal polypep
c	11	32.2	23.3	138	14	AAO38648	Encodes antifungal
c	12	30.4	22.0	37948	20	AAZ06831	Phototaxis lumin
c	13	30	21.7	2172	24	AAZ06853	CDNA sequence #440
c	14	29	21.0	276	16	AAZ24882	Human gene signatu
c	15	29	21.0	1937	24	AAZ62577	CDNA sequence #364
c	16	29	21.0	1082138	21	AAZ22305	Arabidopsis thalia
c	17	28.8	20.9	15109	18	AAV74355	Staphylococcus aur
c	18	28.6	20.7	1024	21	AAZ41895	Arabidopsis thalia
c	19	28.6	20.7	1400	21	AAZ15484	16S rRNA sequence
c	20	28.6	20.7	1446	21	AAZ15485	Treponema palladiu
c	21	28.6	20.7	1544	22	AAZ11030	Human bradykinin r
c	22	28.6	20.7	7328	21	AAZ20874	Human bradykinin r
c	23	28.6	20.7	7328	21	AAZ20878	Human bradykinin r
c	24	28.6	20.7	7328	21	AAZ20887	Human bradykinin r
c	25	28.6	20.7	7328	21	AAZ34752	Human adenosine re
c	26	28.6	20.7	7328	21	AAZ34756	Human adenosine re
c	27	28.6	20.7	7328	21	AAZ34765	Human adenosine re
c	28	28.6	20.7	48333	21	AAZ21451	Human bradykinin r
c	29	28.6	20.7	117609	21	AAZ21435	Human receptor-rel
c	30	28.4	20.6	1277	24	AAZ50367	Human vascular epi
c	31	28.4	20.6	1418	21	AAZ59660	Human secreted pro
c	32	28.4	20.6	2432	22	AAH17679	Human CDNA sequenc
c	33	28.4	20.6	4504	23	ABZ25672	Drosophila melanog
c	34	28.4	20.6	5414	23	ABZ25674	Drosophila melanog
c	35	28.2	20.4	2997	17	AAZ11641	Murine osteogenic
c	36	28.2	20.4	2997	21	AAZ59899	Murine OP-1 downst
c	37	28	20.3	1503800	22	AAZ95240	Human neureregulin-1
c	38	28	20.3	1503900	22	AAZ95733	Human neureregulin-1
c	39	27.6	20.0	342	24	ABZ67413	Listeria innocua D
c	40	27.6	20.0	2539	24	ABZ99857	Mouse ischaemic co
c	41	27.6	20.0	2927	23	ABZ13302	Drosophila melanog
c	42	27.6	20.0	5220	23	ABZ28025	Drosophila melanog
c	43	27.6	20.0	8440	23	ABZ28024	Drosophila melanog
c	44	27.6	20.0	32249	22	AAZ04676	Human reproductive
c	45	27.6	20.0	32249	23	ABZ97583	Human testicular a

ALIGNMENTS

RESULT 1	AAV39187	standard; DNA; 250 BP.
ID	AAV39187;	
AC	AAV39187;	
XX		
DT	25-SEP-1998 (first entry)	
XX		
DE	Alfalfa plant antifungal polypeptide AlfAlFp1 encoding DNA.	
XX		
KW	Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;	
KW	plant pathogenic fungus; AlfAlFp1; AlfAlFp2; ds.	
XX		
OS	Medicago sativa.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	105..242
FT		/tag= a
FT		/product= "mature AlfAlFp1"
PN	MO9826083-A1.	
PD	18-JUN-1998.	
XX		
PF	11-DEC-1997;	97WO-US22662.
XX		
PR	13-DEC-1996;	96US-0766355.
XX		
PA	(MONS) MONSANTO CO.	
XX		
XX	Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;	
PI		
XX		

Query	121	TGTACTAAAGATGTTAA	138
Db	225	TGTACTAAAGATGTTAA	242
Qy	1	AGAACATGTGAGAAATTTGGCAGATTAATATATAGGGAGCCATGCTTTAGTGTGTGACACT	60
Dy	105	AGAACATGTGAGAAATTTGGCAGATTAATATATAGGGAGCCATGCTTTAGTGTGTGACACT	164
Qy	61	CACATGCACACACCAAGAGACGACAGTGTAGTGAAGAGTGTAGGAGACACTTCCGTCGCTGG	120
Dy	165	CACATGCACACCAAGAGAGACGACATTTGTGAAGTGTAGGAGACACTTCCGTCGCTGG	224
Qy	121	TGTACTAAAGATGTTAA	138
Dy	225	TGTACTAAAGATGTTAA	242

RESULT 2

AAV39186

AAV39186 standard; DNA: 490 BP.

AAV39186;

01-OCF-1998 (first entry)

Anti-fungal polypeptide AlfaFP1 encoding cDNA.

Anti-fungal polypeptide; alfalfa plant; Medicago; fungal resistance;

plant pathogenic fungus; AlfaFP1; AlfaFP2; ss.

Medicago sativa.

Key

CDS

Location/Qualifiers

75..293

/*tag= a

/transl_except= (pos:129..131, aa:Glu)

/product= "AlfaFP1 polypeptide"

75..155

/*tag= b

156..290

/*tag= c

[illegible]

KW	plant pathogenic fungus; AlfAFP1; AlfAFP2; ds.
XX	
OS	Medicago sativa.
XX	
FH	Key
FT	Location/Qualifiers
FT	173..310
FT	/tag= a
FT	/product= "mature AlfAFP1"
PN	
XX	WO9826083-AI.
PD	
PD	18-JUN-1998.
XX	
PF	11-DEC-1997; 97WO-US22662.
XX	
PR	13-DEC-1996; 96US-076635.
XX	
PA	(MONS) MONSANTO CO.
PI	
PI	Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;
XX	
DR	WI: 1998-348537/30.
DR	P-PSDB: AAM61964.
XX	
PT	Antifungal poly(peptide(s) and genes isolated from alfalfa plant(s)
PT	- used to control plant pathogenic fungi and to produce transformed
PT	plants with increased fungal resistance
XX	
PS	Claim 5; Page 77; 97pp; English.
XX	
CC	This DNA encodes an antifungal polypeptide, AlfAFP1 isolated from
CC	alfalfa plants (Medicago). The polypeptides AlfAFP1 and AlfAFP2 are
CC	useful to control plant fungi, especially pathogenic fungi, by
CC	transforming plant cells with a vector comprising sequences encoding
CC	AlfAFP1 or AlfAFP2 to allow expression of antifungally effective amounts
CC	of the polypeptide. Such transformed plants may be e.g. apple, wheat,
CC	cotton and especially potato. Micro-organisms may also be transformed
CC	to produce the polypeptides, and applied to plants to control plant
CC	fungi. The polypeptides can also be included with a suitable solvent in
CC	antifungal compositions and these can be administered to plants to
CC	control plant fungi. Such compositions and genetically engineered plants
CC	may also contain additional molecules e.g. the compositions can contain
CC	other antifungal agents or the plants contain DNA encoding insecticidal
CC	(e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful
CC	to prepare antibodies useful to detect polypeptides or isolate other
CC	alfalfa plant antifungal protein antigens. The nucleic acids are useful
CC	to produce polypeptides and transgenic plants and as probes or primers in
CC	nucleic acid hybridisation e.g. to detect complementary sequences in
CC	samples, and to prepare mutants or isolate similar sequences from related
CC	species.
XX	
SO	Sequence 507 BP; 181 A; 85 C; 102 G; 136 T; 3 other;
	Query Match 100.0%; Score 138; DB 19; Length 507;
	Best Local Similarity 100.0%; Pred. No. 1.7e-35;
	Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 AGAAGATGTGGAATTGGCAGATAAAATATTAGGGGCACATGCTTATAGTGTTGTGCACT 60
Db	173 AGAACATGTGCAAAATTTGGCATTAATATATAGGGGCCATGCTTATAGTGTTGTGCACT 232
OY	61 CACTGCACAACCMAAGAGAAGACGCACTTAGTGGAAGGTGTAGGAGACACTTCGCTCGTG 120
Db	233 CACTGCACAACCAAGAGAAGACGCACTTAGTGGAAGGTGTAGGAGACACTTCGCTCGTG 292
OY	121 TGTTCTAAAAGATGTTAA 138
Db	293 TGTTCTAAAAGATGTTAA 310

XX	AAY39190;
AC	
XX	
DT	25-SEP-1998 (first entry)
XX	
DE	Antifungal polypeptide AlfAFP2 5' region.
XX	
KW	Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
RW	plant pathogenic fungus; AlfAFP1; AlfAFP2; ds.
OS	
XX	Medicago sativa.
PN	
PD	MO9826083-Al.
XX	
PD	18-JUN-1998.
PF	
XX	11-DEC-1997; 97MO-US22662.
XX	
FR	13-DEC-1996; 96US-0766355.
XX	
PA	(MONS) MONSANTO CO.
XX	
PI	Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;
DR	WPI; 1998-348537/30.
XX	
PX	Antifungal poly(peptide(s) and genes isolated from alfalfa plant(s)
PT	- used to control plant pathogenic fungi and to produce transformed
PT	plants with increased fungal resistance
XX	
XX	Claim 18; Page 75; 97pp; English.
XX	
CC	This sequence represents the 5' region of the DNA encoding an antifungal
CC	polypeptide, AlfAFP2 isolated from alfalfa plants (Medicago). The
CC	polypeptides AlfAFP1 and AlfAFP2 are useful to control plant fungi,
CC	especially pathogenic fungi, by transforming plant cells with a vector
CC	comprising sequences encoding AlfAFP1 or AlfAFP2 to allow expression of
CC	antifungally effective amounts of the polypeptide. Such transformed
CC	plants may be e.g. apple, wheat, cotton and especially potato.
CC	Micro-organisms may also be transformed to produce the polypeptides, and
CC	applied to plants to control plant fungi. The polypeptides can also be
CC	included with a suitable solvent in antifungal compositions and these can
CC	be administered to plants to control plant fungi. Such compositions and
CC	genetically engineered plants may also contain additional molecules e.g.
CC	the compositions can contain other antifungal agents or the plants
CC	contain DNA encoding insecticidal (e.g. Bacillus thuringiensis)
CC	proteins. The polypeptides are also useful to prepare antibodies useful
CC	to detect polypeptides or isolate other alfalfa plant antifungal protein
CC	antigens. The nucleic acids are useful to produce polypeptides and
CC	transgenic plants and as probes or primers in nucleic acid hybridisation
CC	e.g. to detect complementary sequences in samples, and to prepare mutants
CC	or isolate similar sequences from related species.
XX	
XX	
SO	Sequence 200 BP; 48 A; 36 C; 65 G; 50 T; 1 other;
	Query Match 86.5%; Score 119.4; DB 19; Length 200;
	Best Local Similarity 99.2%; Pred. No. 5.7e-33;
	Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY	1 AGACATGTGAGCAATTGGCAGATAAATATGAGGGACCATCGCTTAGTGGTTGTGCACACT 60
Dd	80 AGAACATGTGAGCAATTGGCAGATAAATATGAGGGACCATCGCTTAGTGGTTGTGCACACT 139
OY	61 CACTGCACAACCMAAGAGAACCAGCACTTAAGTGGAAGGTGTAGGAGAGACACTCCGCCCTCTGG 120
Dd	140 CACTGCACAACCMAAGAGAACCAGCACTTAAGTGGAAGGTGTAGGAGAGACACTCCGCCCTCTGC 199
OY	121 T 121
Dd	200 T 200

AAV39194
ID AAV39194 standard; DNA; 327 BP.
XX
AC AAV39194;
XX
DT 25-SEP-1998 (first entry)
XX
DE Antifungal polypeptide AlfaFP2 3' region.
XX
KW Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
XX plant pathogenic fungus; AlfaFP1; AlfaFP2; ds.
XX
OS Medicago sativa.
XX
PN WO9826083-A1.
XX
PD 18-JUN-1998.
XX
PF 11-DEC-1997; 97WO-US22662.
XX
PR 13-DEC-1996; 96US-0766355.
XX
PA (MONS) MONSANTO CO.
XX
PI Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;
XX WPI: 1998-348537/30.
XX
PT Antifungal polypeptide(s) and genes isolated from alfalfa plant(s)
PT - used to control plant pathogenic fungi and to produce transformed
PT plants with increased fungal resistance
XX
PS Claim 18; Page 77; 97pp; English.
XX
CC This sequence represents the 3' region of the DNA encoding an antifungal
CC polypeptide, AlfaFP2 isolated from alfalfa plants (Medicago). The
CC polypeptides AlfaFP1 and AlfaFP2 are useful to control plant fungi,
CC especially pathogenic fungi, by transforming plant cells with a vector
CC comprising sequences encoding AlfaFP1 or AlfaFP2 to allow expression of
CC antifungally effective amounts of the polypeptide. Such transformed
CC plants may be e.g. apple, wheat, cotton and especially potato.
CC Micro-organisms may also be transformed to produce the polypeptides, and
CC applied to plants to control plant fungi. The polypeptides can also be
CC included with a suitable solvent in antifungal compositions and these can
CC be administered to plants to control plant fungi. Such compositions and
CC genetically engineered plants may also contain additional molecules e.g.
CC the compositions can contain other antifungal agents or the plants
CC contain DNA encoding insecticidal (e.g. Bacillus thuringiensis)
CC proteins. The polypeptides are also useful to prepare antibodies useful
CC to detect polypeptides or isolate other alfalfa plant antifungal protein
CC antigens. The nucleic acids are useful to produce polypeptides and
CC transgenic plants and as probes or primers in nucleic acid hybridisation
CC e.g. to detect complementary sequences in samples, and to prepare mutants
CC or isolate similar sequences from related species.
XX
SQ Sequence 327 BP; 125 A; 49 C; 60 G; 91 T; 2 other;

Query Match 85.4%; Score 117.8; DB 19; Length 327;
Best Local Similarity 94.6%; Pred. No. 2.6e-32;
Matches 122; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

YY 10 GAGAAATTTGGCAGATAATATATAGGGGACATGCTTACTGCTTGACACTGACAC 69
DB 1 GAGAAATTTGGCGATTAAGTATAGGGGACATGCTTACTGCTTGACACTGACAC 60
YY 70 ACCAAAGAGACGAGTAGTGGAAGGTGTAGGACACCTCCGCTGCTGTACTTAA 129
DB 61 ACCAAAGAGACGAGTAGTGGAAGGTGTAGGACCTTCTGTGTACTTAA 120
YY 130 AGATGTTAA 138
DB 121 AGATGTTAA 129

RESULT 6
AAZ49412
ID AAZ49412 standard; CDNA; 468 BP.
XX
AC AAZ49412;
XX
DT 04-APR-2000 (first entry)
XX
DE Pea Defensin protein Drr230, encoding CDNA.
XX
KW Transgenic plant; disease resistance; DRR206; defensin; Drr230; PR10.1;
KW chitinase; recombinant expression system; Pea; Canola; Blackleg fungus;
KW CaMY 35S inducible promoter; T-DNA; bacterial/fungal pathogen;
KW Leptosphaeria maculans; Rhizoctonia solani; Sclerotinia sclerotiorum; ds.
XX
OS Pisum sativum.
XX
PN WO200001824-A2.
XX
PD 13-JAN-2000.
XX
PF 02-JUL-1999; 99WO-CA00608.
XX
PR 03-JUL-1998; 98CA-2242116.
PR 06-JUL-1998; 98US-0091751.
XX
PA (UYMA-) UNIV MANITOBA.
XX
PI Fristensky B, Wang Y;
XX WPI: 2000-126938/11.
XX P-PSDB: AAV44509.
XX
PT Recombinant expression system for expressing DRR206 or defensin, used
PT to produce pathogen resistant Brassica napus
XX
PS Claim 11; Fig 9; 39pp; English.
XX
CC The present sequence is the CDNA encoding defensin protein, derived from
CC the clone Drr230 of Pea. This sequence is strongly induced by bacterial
CC and fungal pathogens like, blackleg fungus. This gene is used in a
CC recombinant expression system, capable of transforming plants like,
CC Canola (Brassica napus), under the constitutive control of CaMY 35S
CC inducible promoter, responsive to pathogen infections. T-DNA sequence is
CC also present, for integration of the expression system into the plant
CC genome. Transgenic plants expressing DRR206 and defensin protein,
CC inhibited fungal growth in-vitro and are resistant to pathogenic
CC infections of Rhizoctonia solani, Leptosphaeria maculans and Sclerotinia
CC sclerotiorum.
XX
SQ Sequence 468 BP; 153 A; 88 C; 84 G; 143 T; 0 other;

Query Match 64.2%; Score 88.6; DB 21; Length 468;
Best Local Similarity 78.5%; Pred. No. 9e-22;
Matches 106; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

YY 4 ACATGTGAGATTTGGCAGATAATATATAGGGGACATGCTTACTGCTTGACACTGAC 63
DB 162 ACATGTGAGATTTGGCTGCTTCAATATAGGAGATGCTTCGCTGATGTGACCGTAC 221
YY 64 TGCACAAACCAAGACGCGAGTAGTGGAAGGTGTAGGACACCTCCGCTGCTGTGT 123
DB 222 TGTAGAACCAAGAGGCGCGCAATTAAGCGGACAGATGCGAGTATGCTTCCCTGTGTGTC 281
YY 124 ACTAAAAGATGTTAA 138

Db 282 ACTAAAACTGTTAA 296

RESULT 7
AAV39191

ID AAV39191 standard; DNA: 293 BP.

XX AAV39191;

DT 25-SEP-1998 (first entry)

DE Antifungal polypeptide AlfaFP2 coding sequence.

KW Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;

KW plant pathogenic fungus; AlfaFP1; AlfaFP2; ds.

OS Medicago sativa.

PN WO9826083-A1.

PD 18-JUN-1998.

PF 11-DEC-1997; 97WO-US22662.

PR 13-DEC-1996; 96US-0766355.

PA (MONS) MONSANTO CO.

PI Haktmi S, Liang J, Rosenberger CA, Shah DM, Wu YS;

DR WPI: 1998-348537/30.

PT Antifungal polypeptide(s) and genes isolated from alfalfa plant(s)
PT - used to control plant pathogenic fungi and to produce transformed
PT plants with increased fungal resistance

PS Claim 18; Page 75; 97pp; English.

CC This represents a coding sequence of an antifungal polypeptide, AlfaFP2
CC isolated from alfalfa plants (Medicago). The polypeptides AlfaFP1 and
CC AlfaFP2 are useful to control plant fungi, especially pathogenic fungi,
CC by transforming plant cells with a vector comprising sequences encoding
CC AlfaFP1 or AlfaFP2 to allow expression of antifungally effective amounts
CC of the polypeptide. Such transformed plants may be e.g. apple, wheat,
CC cotton and especially potato. Micro-organisms may also be transformed
CC to produce the polypeptides, and applied to plants to control plant
CC fungi. The polypeptides can also be included with a suitable solvent in
CC antifungal compositions and these can be administered to plants to
CC control plant fungi. Such compositions and genetically engineered plants
CC may also contain additional molecules e.g. the compositions can contain
CC other antifungal agents or the plants contain DNA encoding insecticidal
CC (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful
CC to prepare antibodies useful to detect polypeptides or isolate other
CC alfalfa plant antifungal protein antigens. The nucleic acids are useful
CC to produce polypeptides and transgenic plants and as probes or primers in
CC nucleic acid hybridisation e.g. to detect complementary sequences in
CC samples, and to prepare mutants or isolate similar sequences from related
CC species.

XX Sequence 293 BP; 82 A; 60 C; 72 G; 77 T; 2 other;

Query Match 62.8%; Score 86.6; DB 19; Length 293;

Best Local Similarity 83.1%; Pred. No. 4e-21; Mismatches 0; Gaps 0;

Matches 98; Conservative 0; Mismatches 20; Indels 0;

OY 4 ACATGTGAGAAATTTGGCAGATAAATATAGGACCATGCTTAGTGGTTGTGACACTCAC 63

DB 176 ACTTGTGAGAAATTTGGCTAACATACATACAGGAGCATGCTTGTGACCTTTCAC 235

OY 64 TCCACAACCAAGAGAACCCACTTGTGAAAGTGTAGGAGAGACTCCGCGCTGCT 121

DB 236 TCCAAAACCAAGAACACTTACTTAGCGGAGGAGGAGACTTCGCGCTGCT 293

RESULT 8
AADI7530

ID AADI7530 standard; CDNA: 494 BP.

XX AADI7530;

DT 10-DEC-2001 (first entry)

DE Soybean gly m2 protein encoding CDNA from clone sls1c.pk027.all.

KW Soybean; allergen; transgenic plant; P34 protein; Gly m Bd 30K; Gly m 1;

KW soybean vacuolar protein; Gly m 1A; Gly m 1B; rGLY m3; Glycinin G1;

KW alabid; food; infant formula; animal feed; coating; salad oil; syrup;

KW spraying oil; roasting oil; frying oil; cracker; confectionery product;

KW snack food; topping; sauce; batter; breading mixture; baking mix; dough;

KW Gly m2 protein; clone sls1c.pk027.all; ss.

OS Glycine max.

PN Key Location/Qualifiers

FT CDS 46..273

FT /tag= a

FT /product= "Soybean gly m2 protein"

PN WO200168887-A2.

PD 20-SEP-2001.

PF 15-MAR-2001; 2001WO-US08254.

PR 16-MAR-2000; 2000US-0189823.

PA (DDPO) DU POINT DE NEMOURS & CO E I.

PI (PION-) PIONEER HI-BRED INT INC.

DR Jung R, Kinney AJ;

DR WPI: 2001-582460/65.

DR P-PSDB; AAE10361.

PT Recombinant expression construct to lower allergen (e.g. Gly m Bd 30K)

PT content of a soybean, comprises a nucleic acid fragment encoding the

PT allergen, useful for producing soybean plants which can be used to make

PT soybean products

PS Example 7; Page 51-52; 57pp; English.

CC The patent discloses hypoallergenic transgenic soybeans and recombinant
CC expression constructs to lower soybean vacuolar protein, commonly known
CC as P34 (Gly m Bd 30K or Gly m 1) and other allergens such as Gly m 1A,
CC Gly m 1B, rGLY m3 or Glycinin G1 (alabid). The allergen content of the
CC soybean is reduced by sense suppression which is accomplished by using
CC the expression construct that comprises a nucleic acid fragment encoding
CC the allergen. The constructs are useful for producing hypoallergenic
CC transgenic soybean plants which can be used to make hypoallergenic
CC soybean products which can be used in a variety of food (e.g. infant
CC formula) and animal feed applications. The oil made from seeds of the
CC hypoallergenic transgenic soybean plants can be used as ingredients,
CC as coatings, as salad oils, as spraying oils, as roasting oils, and
CC as frying oils. The foods in which the oil may be used include crackers
CC and snack foods, confectionery products, syrups and toppings, sauces,
CC batter and breading mixtures, baking mixes and doughs. The present
CC sequence is soybean Gly m2 protein encoding CDNA from sls1c.pk027.all
CC clone. This sequence is a minor soybean seed allergen.

XX Sequence 494 BP; 153 A; 97 C; 103 G; 134 T; 7 other;

Query Match 44.5%; Score 61.4; DB 22; Length 494;

Best Local Similarity 70.2%; Pred. No. 5.4e-12; Mismatches 36; Indels 6; Gaps 1;

Matches 99; Conservative 0; Mismatches 36; Indels 6; Gaps 1;

OY 4 ACATGTGAGATTTGGCAGATAAATATAGGGACCATGCT-----TAGTGTGTGTGAC 57
DB 133 ACTTGGGAGACCTGCTGCTATATACAGGGTCCATGCTGACCATGCGCAT 192
OY 58 ACTCACTGCACCAACCAAGAGACGAGTGTAGGAGAGGAGTGTGCGCTGC 117
DB 193 GATCACTGCAAGAACCAAGAGCATTTGCTCAGACGACATGACAGGAGCATTTGCTGT 252
OY 118 TGGTGTACTAAAGATGTTAA 138
DB 253 TGGTGCACCAAAAACCTGTAA 273

RESULT 9

AAQ70126
ID AAQ70126 standard; cDNA; 141 BP.

XX AAQ70126;

XX 14-FEB-1995 (first entry)

DE Antimicrobial Lc-AFP.

XX Antimicrobial; Lc-AFP; symbiosis; disease-resistance;

KW fungus-resistance; Clavibacter xyli subsp. cynodontis; CXC;

KW crop improvement; endophyte; ss.

OS Lathyrus cicerca.

XX MO9416076-A.

XX 21-JUL-1994.

XX 05-JAN-1994; 94WO-GB00012.

XX 08-JAN-1993; 93GB-0000281.

XX (ZENE) ZENECA LTD.

XX Dubock AC, Powell KA, Rees SB;

XX WPI; 1994-249223/30.

DR P-PSDB; AAR57322.

XX Antimicrobial protein producing endo-symbiotic microorganisms -

PT is produced by combining nucleic acids encoding the protein with

PT an endophyte, useful for protecting plant hosts from esp. fungal

PT disease

XX PS Disclosure; Page 30; 39pp; English.

XX Plant-derived antimicrobial proteins are expressed in endosymbiotic

CC Clavibacter xyli subsp. cynodontis (CXC). Plants or seeds treated

CC with recombinant CXC are protected against fungal disease. A

CC suitable antimicrobial protein is Lc-AFP from L. cicerca. A

CC possible predicted sequence for the Lc-AFP gene is given in AAQ70126.

XX Sequence 141 BP; 43 A; 30 C; 32 G; 33 T; 3 other;

SO Query Match 29.0%; Score 40; DB 15; Length 141;

Best Local Similarity 60.6%; Pred. No. 0.00017;

Matches 83; Conservative 0; Mismatches 48; Indels 6; Gaps 1;

DB 124 TGGTGCACCTAGAACTG 140

RESULT 10

AAV39197/C

ID AAV39197 standard; DNA; 47 BP.

XX AAV39197;

XX 25-SEP-1998 (first entry)

DE Antifungal polypeptide AlfaFP2 3' gene specific primer.

XX Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;

KW plant pathogenic fungus; AlfaFP1, AlfaFP2; PCR primer; ss.

XX Synthetic.

OS Medicago sativa.

XX WO9826083-A1.

XX 18-JUN-1998.

XX 11-DEC-1997; 97WO-US22662.

XX 13-DEC-1996; 96US-0766355.

XX (MONS) MONSANTO CO.

XX Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;

XX WPI; 1998-348537/30.

XX Antifungal polypeptide(s) and genes isolated from alfalfa plant(s)

PT - used to control plant pathogenic fungi and to produce transformed

PT plants with increased fungal resistance

XX Example 4; Page 78; 97pp; English.

XX This primer is used for the PCR amplification of the cDNA encoding an

CC antifungal polypeptide, AlfaFP2. The antifungal polypeptides AlfaFP1 and

CC AlfaFP2 isolated from alfalfa plants (Medicago) are useful to control

CC plant fungi, especially pathogenic fungi, by transforming plant cells

CC with a vector comprising sequences encoding AlfaFP1 or AlfaFP2 to allow

CC expression of antifungally effective amounts of the polypeptide. Such

CC transformed plants may be e.g. apple, wheat, cotton and especially

CC potato. Micro-organisms may also be transformed to produce the

CC polypeptides, and applied to plants to control plant fungi. The

CC compositions and these can be administered to plants to control plant

CC fungi. Such compositions and genetically engineered plants may also

CC contain additional molecules e.g. the compositions can contain other

CC (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful

CC to prepare antibodies useful to detect polypeptides or isolate other

CC alfalfa plant antifungal protein antigens. The nucleic acids are useful

CC to produce polypeptides and transgenic plants and as probes or primers in

CC nucleic acid hybridisation e.g. to detect complementary sequences in

CC samples, and to prepare mutants or isolate similar sequences from related

XX Species.

XX Sequence 47 BP; 11 A; 13 C; 11 G; 12 T; 0 other;

SO Query Match 28.3%; Score 39; DB 19; Length 47;

Best Local Similarity 100.0%; Pred. No. 0.00026;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 100 AGGAGACACTTCCGCTGCTGTGACTAAAGATGTTAA 138

DB 47 AGGAGACACTTCCGCTGCTGTGACTAAAGATGTTAA 9

RESULT 11

```

AA038648
ID AA038648 standard; DNA; 138 BP.
XX
AC AA038648;
XX
DT 07-JUL-1993 (first entry)
XX
DE Encodes antifungal protein Lc-Afp1.
XX
KW Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria;
KW fungicide; bactericide; antibiotic; antifungal; gram positive;
XX plant disease resistance; low toxicity.
XX
OS Lathyrus ciceria.
XX
FH Key Location/Qualifiers
FT CDS 1..138
FT /*tag= a
XX
PN W09305153-A.
PD 18-MAR-1993.
XX
PF 27-AUG-1992; 92WO-GB01570.
XX
PR 29-AUG-1991; 91GB-0018523.
PR 13-FEB-1992; 92GB-0003038.
PR 25-JUN-1992; 92GB-0013526.
XX
PA (ICIL ) IMPERIAL CHEM IND PLC.
XX
PI Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;
PI Vanderleyden J;
XX
DR WPI: 1993-100978/12.
XX
XX Biofidal proteins isolated from seeds of plants - e.g. brassica
XX or dahlia, useful for increasing plants' resistance to fungal and
XX bacterial diseases
XX
PS Disclosure: Flg 31A; 110pp; English.
XX
CC This sequence appears to encode antifungal protein Lc-Afp1 from
CC Lathyrus ciceria - see AAR33760. The exact source and isolation of the
CC sequence is unclear from the specification.
XX
SQ Sequence 138 BP; 43 A; 30 C; 32 G; 33 T; 0 other;
XX
Query Match 23.3%; Score 32.2; DB 14; Length 138;
Best Local Similarity 58.8%; Pred. No. 0.11;
Matches 77; Conservative 0; Mismatches 48; Indels 6; Gaps 1;
XX
OY 4 ACATGTGAGAAATTTGGCAGATAAATATAGGACCATGCTTAGTGT-----TGTGAC 57
DB 4 ACTTTCGAGAACCTTTCTGCACTTTCAGAGGACCATGATCCAGATGGAACATGCAC 63
OY 58 ACTCACTGCACACCAAGAGAACGACATTAGTGAAGGTGAGGACACTTCGCTGC 117
DB 64 AAGCATTTGCAGAACACAGACATCTTCTTCTGGAAGATGACAGATGATTTCTGCTGG 123
OY 118 TGTGTACTAA 128
DB 124 TGCACCTAGAAA 134

```

```

DE Photorhabdus luminescens 38kb DNA fragment.
XX
KW Symbiotic bacterium; nematode; insect; larva; toxin;
KW insecticide; ds.
XX
OS Photorhabdus luminescens.
XX
FH Key Location/Qualifiers
FT CDS 66..1898
FT /*tag= a
FT /partial
FT /label=orf7
FT 2416..9909
FT /*tag= b
FT /label= hph3
FT complement (2817..3395)
FT /*tag= c
FT /label= orf18
FT 9966..14633
FT /*tag= d
FT /label= orf4
FT 14699..15007
FT /*tag= e
FT /label= orf19
FT 15171..18035
FT /*tag= f
FT /label= orf5
FT /product= "Insecticidal toxin"
FT complement (17072..17398)
FT /*tag= g
FT /label= orf22
FT complement (18235..19167)
FT /*tag= h
FT /label= orf10
FT complement (19385..20116)
FT /*tag= i
FT /label= orf14
FT complement (20217..20963)
FT /*tag= j
FT /label= orf13
FT complement (22172..23086)
FT /*tag= k
FT /label= orf11
FT 23768..31336
FT /*tag= l
FT /label= hph2
FT /product= "Insecticidal toxin"
FT 31393..35838
FT /*tag= m
FT /label= orf2
FT /product= "Insecticidal toxin"
FT complement (35383..35709)
FT /*tag= n
FT /label= orf21
FT complement (36032..36661)
FT /*tag= o
FT /label= orf16
FT complement (36654..37781)
FT /*tag= p
FT /label= orf8
XX
PN W09942589-A2.
XX
PD 26-AUG-1999.
XX
PF 18-FEB-1999; 99WO-EP01015.
XX
PR 20-JAN-1999; 99US-0116439.
PR 20-FEB-1998; 98US-0027080.
XX
PA (NOVS ) NOVARTIS AG.
XX (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.

```

[illegible]

PT for diagnosis of abnormal cell function, by preparing cDNA that
PT reflects relative abundance of corresp. mRNA in specific human
tissues

PS Claim 1; Page 1718; 2245pp; Japanese.

XX
CC A single-stranded DNA (or its complementary strand or the corresp.
CC double-stranded DNA) which comprises one of the 7837 "GS" sequences
CC given in AAT19001-T26837 and which is able to hybridise to part of
CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
CC sequences were obtained from 3'-directed cDNA libraries prepared
CC from various human tissues; synthesis of cDNA was initiated from the
CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
CC untranslated sequence is unique to a particular mRNA species, almost
CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC is constructed so as to reflect accurately the relative abundance of
CC different mRNAs in the particular tissue from which it was derived.
CC The appearance frequency of a given GS in a cDNA library can be
CC determined (esp. using primers and probes derived from the GS
CC sequences) as a means of diagnosing abnormal cell function or for
CC recognising different cell types.

SQ Sequence 276 BP; 85 A; 50 C; 61 G; 66 T; 14 other;

Query Match 21.0%; Score 29; DB 16; Length 276;
Best Local Similarity 55.2%; Pred. No. 1.9;
Matches 53; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

OY 3 AACATGTGAGATTGGCAGATAATATAGGAGCAGTCCTTAGTGGTTGTGACACTCA 62

DB 218 AATATATCTTAACTCTGCGGNAATATACGTATGCCATTTCTTAATATCAGACAGA 159

OY 63 CTCGACACCAAGAGAGAGCAGTCTAGTGTGAAGTG 98

DB 158 CTGACTCAAAATTAAGAGAGTCTGTGCAGATG 123

RESULT 15

AAS62577

ID AAS62577 standard; cDNA; 1937 BP.

AC AAS62577;

DT 14-FEB-2002 (first entry)

XX cDNA sequence #364 encoding novel human secreted protein.

KW Human secreted protein; hyperproliferative disorder; autoimmune disorder;

KW immune deficiency disorder; blood disorder; inflammatory disorder;

KW infectious disorder; gene therapy; antimicrobial; hepatotropic;

XX immunosuppressive; antirheumatic; ss.

OS Homo sapiens.

XX WO200177291-A2.

PD 18-OCT-2001.

PF 29-MAR-2001; 2001WO-US10485.

PR 06-APR-2000; 2000US-195604P.

XX (GEM) GENETICS INST INC.

PI Wong GG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ,

XX Gulukota K, Graham JR;

DR WPI; 2002-010900/01.

XX New polynucleotides encoding secreted proteins useful for treating e.g.
PT asthma, HIV and Crohn's disease -
XX Claim 1; Page 267; 391pp; English.

XX The present invention relates to the isolation of novel cDNA sequences
CC which encode human secreted proteins. The cDNA sequences have been
CC derived from a variety of human tissues. The invention also provides
CC a method for producing proteins from these polynucleotide sequences.
CC The proteins are useful for identifying compounds that modulate their
CC activity and production, and the cell is also useful for identifying
CC compounds that modulate expression of the polynucleotide sequences
CC encoding the secreted proteins. The sequences of the invention are
CC useful for treating diseases such as hyperproliferative disorders
CC (e.g. cancer), immune deficiency disorders (e.g. severe combined
CC immunodeficiency (SCID)), autoimmune disorders (e.g. multiple
CC sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory
CC disorders (e.g. arthritis) and infectious disorders (e.g. hepatitis).
CC The polynucleotide sequences of the invention are also useful in gene
CC therapy. AAS62214-AAS62838 represent the cDNA sequences of the
CC invention that encode for novel human secreted proteins.

SQ Sequence 1937 BP; 613 A; 304 C; 309 G; 711 T; 0 other;

Query Match 21.0%; Score 29; DB 24; Length 1937;
Best Local Similarity 57.0%; Pred. No. 3.8;
Matches 53; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

OY 15 TTGGCAGATAAATATAGGAGCAGTCCTTAGTGGTTGTGACACTGCACACCA 74

DB 891 TTGTATTAATAGTGAAGGACAAATGTTAAAGGCTAAGATAATTCCTGCAAAAGGAC 950

OY 75 AGAGAAGCAGTTAGTGAAGGCTAGAGGACGA 107

DB 951 ACAGAAGGAGCTCTTAAGAAGATGAATGATGA 983

Search completed: May 8, 2003, 05:54:07
Job time : 84.9108 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2003, 05:54:13 ; Search time 16.2611 Seconds

(without alignments)
2602.608 Million cell updates/sec

Title: US-10-010-731-13_COPY_105_242

Perfect score: 138

Sequence: 1 AGACATGTGAGAAATTTGGC.....GGTGTACTAAAGATGTAA 138

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapept 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued_Patents_NA.*

2: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*

3: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*

5: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*

6: /cgn2_6/ptodata/1/ina/PTCUTS.COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	100.0	250	3	US-08-766-355-13 Sequence 13, Appl
2	138	100.0	250	4	US-09-003-198A-13 Sequence 13, Appl
3	138	100.0	250	4	US-09-428-805-13 Sequence 13, Appl
4	138	100.0	490	4	US-09-003-198A-19 Sequence 19, Appl
5	138	100.0	507	3	US-08-766-355-10 Sequence 10, Appl
6	138	100.0	507	4	US-09-003-198A-10 Sequence 10, Appl
7	138	100.0	507	4	US-09-428-805-10 Sequence 10, Appl
8	120.8	87.5	189	4	US-09-003-198A-18 Sequence 18, Appl
9	119.4	86.5	200	3	US-08-766-355-5 Sequence 5, Appl
10	119.4	86.5	200	4	US-09-003-198A-5 Sequence 5, Appl
11	119.4	86.5	200	4	US-09-428-805-5 Sequence 5, Appl
12	117.8	85.4	327	4	US-08-766-355-9 Sequence 9, Appl
13	117.8	85.4	327	4	US-09-003-198A-9 Sequence 9, Appl
14	117.8	85.4	327	4	US-09-428-805-9 Sequence 9, Appl
15	86.6	62.8	293	4	US-08-766-355-6 Sequence 6, Appl
16	86.6	62.8	293	4	US-09-003-198A-6 Sequence 6, Appl
17	86.6	62.8	293	4	US-09-428-805-6 Sequence 6, Appl
18	40	29.0	141	1	US-08-377-687-35 Sequence 35, Appl
19	40	29.0	141	1	US-08-777-192-35 Sequence 35, Appl
20	40	29.0	141	1	US-08-971-982-35 Sequence 35, Appl
21	39	28.3	47	4	US-08-766-355-12 Sequence 12, Appl
22	39	28.3	47	4	US-09-003-198A-12 Sequence 12, Appl
23	39	28.3	47	4	US-09-428-805-12 Sequence 12, Appl
24	30.4	22.0	37948	4	US-09-251-645-11 Sequence 11, Appl
25	28.6	20.7	1400	3	US-09-191-099-7 Sequence 7, Appl
26	28.6	20.7	1446	3	US-09-191-099-8 Sequence 8, Appl
27	28.2	20.4	2997	3	US-08-486-343A-3 Sequence 3, Appl

c	28	28.2	20.4	2997	5	PCT-US95-07349-3	Sequence 3, Appl
c	29	27.6	20.0	1231	4	US-09-015-188-5	Sequence 5, Appl
c	30	25.8	18.7	1212	2	US-09-092-770-18	Sequence 18, Appl
c	31	25.8	18.7	1212	4	US-09-222-851-18	Sequence 18, Appl
c	32	25.8	18.7	1215	2	US-09-092-770-8	Sequence 8, Appl
c	33	25.8	18.7	1215	2	US-09-222-851-8	Sequence 8, Appl
c	34	25.4	18.4	1366	3	US-09-191-099-4	Sequence 4, Appl
c	35	25.4	18.4	1413	3	US-09-191-099-1	Sequence 1, Appl
c	36	25.4	18.4	1462	3	US-09-191-099-3	Sequence 3, Appl
c	37	25.4	18.4	1503	4	US-08-943-571-1	Sequence 1, Appl
c	38	25.4	18.4	1589	4	US-09-464-483-1	Sequence 1, Appl
c	39	25.4	18.4	1589	4	US-09-414-664-1	Sequence 1, Appl
c	40	25.4	18.4	1842	4	US-09-832-498-1	Sequence 1, Appl
c	41	25.4	18.4	1842	4	US-09-832-614A-1	Sequence 1, Appl
c	42	25.4	18.4	3791	3	US-09-377-310-1	Sequence 1, Appl
c	43	25.4	18.4	4614	1	US-08-325-267A-1	Sequence 1, Appl
c	44	25.4	18.4	15225	2	US-08-892-403A-2	Sequence 2, Appl
c	45	25.4	18.4	62804	4	US-09-800-960-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-766-355-13
Sequence 13, Application US/08766355
Patent No. 6121436
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakim, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 77210
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,355
FILING DATE: Concurrently Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT:063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-766-355-13
Query Match 100.0% Score 138; DB 3; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.5e-42;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 AGACATGTGAGAAATTTGGCAGATAATATPAGGAGCAGATGCTTATAGTGTGTGACACT 60
|||||

Db 105 AGACATGTGAGAAATTTGGCAGATAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 164
QY 61 CACTGCACACCAAGAGACGCACTAGTGAAGGTGTAGGAGCACTTCGGCTGTGG 120
Db 165 CACTGCACACCAAGAGACGCACTAGTGAAGGTGTAGGAGCACTTCGGCTGTGG 224
QY 121 TGTACTAAAGATGTAA 138
Db 225 TGTACTAAAGATGTAA 242

RESULT 2

US-09-003-198A-13
; Sequence 13, Application US/09003198A
; Patent No. 6316407
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip Maganlal
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; APPLICANT: Hakimi, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/003,198A
; FILING DATE: 07-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 787-1400
; TELEFAX: (713) 787-1440
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-003-198A-13

Query Match 100.0%; Score 138; DB 4; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.5e-42;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGACATGTGAGAAATTTGGCAGATAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 60
Db 105 AGACATGTGAGAAATTTGGCAGATAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 164
QY 61 CACTGCACACCAAGAGACGCACTAGTGAAGGTGTAGGAGCACTTCGGCTGTGG 120
Db 165 CACTGCACACCAAGAGACGCACTAGTGAAGGTGTAGGAGCACTTCGGCTGTGG 224
QY 121 TGTACTAAAGATGTAA 138
Db 225 TGTACTAAAGATGTAA 242

RESULT 3

US-09-428-805-13
; Sequence 13, Application US/09428805
; Patent No. 6329504
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip Maganlal
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; APPLICANT: Hakimi, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 77210
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/428,805
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/766,355
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MOBT:063
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-428-805-13

Query Match 100.0%; Score 138; DB 4; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.5e-42;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGACATGTGAGAAATTTGGCAGATAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 60
Db 105 AGACATGTGAGAAATTTGGCAGATAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 164
QY 61 CACTGCACACCAAGAGACGCACTAGTGAAGGTGTAGGAGCACTTCGGCTGTGG 120
Db 165 CACTGCACACCAAGAGACGCACTAGTGAAGGTGTAGGAGCACTTCGGCTGTGG 224
QY 121 TGTACTAAAGATGTAA 138
Db 225 TGTACTAAAGATGTAA 242

RESULT 4

US-09-003-198A-19
; Sequence 19, Application US/09003198A
; Patent No. 6316407
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip Maganlal
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; APPLICANT: Hakimi, Salim

```

; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESS: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/003,198A
; FILING DATE: 07-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 787-1400
; TELEFAX: (713) 787-1440
; INFORMATION FOR SEQ. ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 490 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; US-09-003-198A-19
;
; Query Match          100.0%; Score 138; DB 4; Length 490;
; Best Local Similarity 100.0%; Pred. No. 2.1e-42;
; Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 AGAACAATGTGAGATTTGGAGATAAATATAGGGAGACATGCTTATGCTGTGACACT 60
; DB 156 AGAACAATGTGAGATTTGGAGATAAATATAGGGAGACATGCTTATGCTGTGACACT 215
; QY 61 CACTGCACAACCAAGAGAACGACGATTAGTGAAGGTGTAGGAGACGACTCCGCTGCTGG 120
; DB 216 CACTGCACAACCAAGAGAACGACGATTAGTGAAGGTGTAGGAGACGACTCCGCTGCTGG 275
; QY 121 TGTACTAAAGATGTTAA 138
; DB 276 TGTACTAAAGATGTTAA 293
;
; RESULT 5
; US-08-766-355-10
; Sequence 10, Application US/08766355
; Patent No. 6121436
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip Maganlal
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; APPLICANT: Hakiml, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 77210
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,355
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MOBT:063
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ. ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 507 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: one-of(17, 424, 485)
; OTHER INFORMATION: /mod_base-OTHER
; OTHER INFORMATION: /note= "N = A or C or G or T"
;
; US-08-766-355-10
;
; Query Match          100.0%; Score 138; DB 3; Length 507;
; Best Local Similarity 100.0%; Pred. No. 2.1e-42;
; Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 AGAACAATGTGAGATTTGGAGATAAATATAGGGAGACATGCTTATGCTGTGACACT 60
; DB 173 AGAACAATGTGAGATTTGGAGATAAATATAGGGAGACATGCTTATGCTGTGACACT 232
; QY 61 CACTGCACAACCAAGAGAACGACGATTAGTGAAGGTGTAGGAGACGACTCCGCTGCTGG 120
; DB 233 CACTGCACAACCAAGAGAACGACGATTAGTGAAGGTGTAGGAGACGACTCCGCTGCTGG 292
; QY 121 TGTACTAAAGATGTTAA 138
; DB 293 TGTACTAAAGATGTTAA 310
;
; RESULT 6
; US-09-003-198A-10
; Sequence 10, Application US/09003198A
; Patent No. 6316407
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip Maganlal
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; APPLICANT: Hakiml, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/003,198A
; FILING DATE: 07-JAN-1998
; CLASSIFICATION:

```

ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 507 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: one-of(17, 424, 485)
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "N" = A or C or G or T"
US-09-003-198A-10

Query Match 100.0%; Score 138; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 2,1e-42;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGACATGTGAGATTGGCAGATAAATATAGGGACCATGCTTTAGTGTGTGACACT 60
|||||
DB 173 AGACATGTGAGATTGGCAGATAAATATAGGGACCATGCTTTAGTGTGTGACACT 232
OY 61 CACTGCACACCAAGAGAACCGAGTTAGTGAAGGTGAGGACACTTCGCTGCTGG 120
|||||
DB 233 CACTGCACACCAAGAGAACCGAGTTAGTGAAGGTGAGGACACTTCGCTGCTGG 292
OY 121 TGTACTAAAAGATGTTAA 138
|||||
DB 293 TGTACTAAAAGATGTTAA 310

RESULT 7
US-09-428-805-10
Sequence 10, Application US/09428805
Patent No. 6329504
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 77210
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/428,805
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/766,355
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT:063

TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 507 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: one-of(17, 424, 485)
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "N" = A or C or G or T"
US-09-428-805-10

Query Match 100.0%; Score 138; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 2,1e-42;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGACATGTGAGATTGGCAGATAAATATAGGGACCATGCTTTAGTGTGTGACACT 60
|||||
DB 173 AGACATGTGAGATTGGCAGATAAATATAGGGACCATGCTTTAGTGTGTGACACT 232
OY 61 CACTGCACACCAAGAGAACCGAGTTAGTGAAGGTGAGGACACTTCGCTGCTGG 120
|||||
DB 233 CACTGCACACCAAGAGAACCGAGTTAGTGAAGGTGAGGACACTTCGCTGCTGG 292
OY 121 TGTACTAAAAGATGTTAA 138
|||||
DB 293 TGTACTAAAAGATGTTAA 310

RESULT 8
US-09-003-198A-18
Sequence 18, Application US/09003198A
Patent No. 6316407
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,198A
FILING DATE: 07-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
US-09-003-198A-18

Query Match
Best Local Similarity 87.5%; Score 120.8; DB 4; Length 189;
Matches 122; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGAACATGTGAGATTGGAGATTAATATAGGGGACCATCTTATGCTGTGACACT 60
DB 63 AGAACATGTGAGATTGGAGATTAATATAGGGGACCATCTTATGCTGTGACACT 122

QY 61 CACTGCACAACCAAGAGAACGCGAGTTAGTGAAGTGTAGGAGCAGCTTCCGCTGCTG 120
DB 123 CACTGCACAACCAAGAGAACGCGAGTTAGTGAAGTGTAGGAGCAGCTTCCGCTGCTG 182

QY 121 TGTG 124
DB 183 TGTG 186

RESULT 9
US-08-766-355-5
Sequence 5, Application US/08766355
Patent No. 6121436
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 77210
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,355
FILING DATE: Concurrently Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT:063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: 17
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "N = A or C or G or T"

US-08-766-355-5

Query Match
Best Local Similarity 86.5%; Score 119.4; DB 3; Length 200;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAACATGTGAGATTGGAGATTAATATAGGGGACCATCTTATGCTGTGACACT 60
DB 80 AGAACATGTGAGATTGGAGATTAATATAGGGGACCATCTTATGCTGTGACACT 139

QY 61 CACTGCACAACCAAGAGAACGCGAGTTAGTGAAGTGTAGGAGCAGCTTCCGCTGCTG 120
DB 140 CACTGCACAACCAAGAGAACGCGAGTTAGTGAAGTGTAGGAGCAGCTTCCGCTGCTG 199

QY 121 T 121
DB 200 T 200

RESULT 10
US-09-003-198A-5
Sequence 5, Application US/09003198A
Patent No. 6316407
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,198A
FILING DATE: 07-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: 17
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "N = A or C or G or T"

US-09-003-198A-5

Query Match
Best Local Similarity 86.5%; Score 119.4; DB 4; Length 200;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAACATGTGAGATTGGAGATTAATATAGGGGACCATCTTATGCTGTGACACT 60
DB 80 AGAACATGTGAGATTGGAGATTAATATAGGGGACCATCTTATGCTGTGACACT 139

QY 61 CACTGCACAACCAAGAGAACGCGAGTTAGTGAAGTGTAGGAGCAGCTTCCGCTGCTG 120
DB 140 CACTGCACAACCAAGAGAACGCGAGTTAGTGAAGTGTAGGAGCAGCTTCCGCTGCTG 199

Db	140	CACGTCACACCAAGAGAAAGCAGTTAGTGGAGGTGTAGGGACGACTTCCGCTGCTGC	199
QY	121	T	121
Db	200	T	200

RESULT 11
 US-09-428-805-5
 : Sequence 5, Application US/09428805
 Patent No. 6329504
 GENERAL INFORMATION:
 APPLICANT: Liang, Jihong
 APPLICANT: Shah, Dilip Maganlal
 APPLICANT: Wu, Yonnie S.
 APPLICANT: Rosenberger, Chndy A.
 APPLICANT: Hakimi, Salim
 TITLE OF INVENTION: Antifungal Polypeptide and Methods for
 TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 77210
 CITY: Houston
 STATE: Texas
 COUNTRY: United States of America
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/428,805
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/766,355
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Kitchell, Barbara S.
 REGISTRATION NUMBER: 33,928
 REFERENCE/DOCKET NUMBER: M087:063
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (512) 474-7577
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 200 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: modified_base
 LOCATION: 17
 OTHER INFORMATION: /mod_base= OTHER
 OTHER INFORMATION: /note= "N" = A or C or G or T"
 US-09-428-805-5

Query Match	86.5%	Score 119.4	DB 4	Length 200
Best Local Similarity	99.2%	Pred. No. 1.3e-35		
Matches 120	Conservative 0	Mismatches 1	Indels 0	Gaps 0

OY	1	AGACATGTGACAAATTGGCAGATTAATATATAGGGACCATGCTTTAGTGTGTCACACT	60
Db	80	AGAAATGTGTGAAATTTGGCAGATTAATAATATAGGGACCATGCTTTAGTGTGTGCACACT	139
OY	61	CACATCACAACCAAGAGAGAACGCAGTTAGTGTGAAGAGTGTAGGGAGACACTCCGTCGCTGG	120
Db	140	CACATCACAACCAAGAGAGAACGCAGTTAGTGTGAAGAGTGTAGGGAGACACTCCGTCGCTCC	199
OY	121	T 121	

```

Db          200 T 200

RESULT 12
US-08-766-355-9
: Sequence 9, Application US/08766355
: Patent No. 6121436
:
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 77210
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,355
FILING DATE: Concurrently Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT-063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 327 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: one-of(244, 305)
OTHER INFORMATION: /mod_base-OTHER
OTHER INFORMATION: /note- "N = A or C or G or T"
US-08-766-355-9

```

```

Query Match      85.4%: Score 117.8; DB 3; Length 327;
Best Local Similarity 94.6%: Pred. No. 6,6e-35;
Matches 122; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      10  GAGAAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGTGTGTGACACTCAGTCGACA 69
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       1  GAGAAATTTGGCGGATTAACATAATAGGGGACCATGCTTTAGTGTGTGTGACACTCAGTCGACA 60

QY      70  ACCAAAGAGAACGCGAGTTAGTGAAGGTGTGTAGGGAGCACTCCGCTGCGTGTACTATA 129
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       61  ACCAAAGAGAACGCGAGTTAGTGAAGGTGTAGGAGGTGTGACTTTCGTTTGTAGTGTACTATA 120

QY      130 AGATGTTAA 138
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       121 AGATGTTAA 129

RESULT 13
US-09-003-198A-9
: Sequence 9, Application US/090003198A
: Patent No. 6316407

```


GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,198A
FILING DATE: 07-Jan-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 327 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: one-of(244, 305)
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "N = A or C or G or T"
US-09-003-198A-9
Query Match 85.4%; Score 117.8; DB 4; Length 327;
Best Local Similarity 94.6%; Pred. No. 6.6e-35;
Matches 122; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 10 GAGAAATTGGCAGATTAATATAGGGGACCATGCTTTAGTGGTGTGACACTGACACTGACA 69
DB 1 GAGAAATTGGCGATAGTATAGGGGACCATGCTTTAGTGGTGTGACACTGACACTGACA 60
QY 70 ACCAAAGAGAACGAGTAGTGAAGGTGAGGAGCAGCTCCGCTGCTGGTACTTAA 129
DB 61 ACCAAAGAGAACGAGTAGTGAAGGTGAGGAGCAGCTCCGCTGCTGGTACTTAA 120
QY 130 AGATGTTAA 138
DB 121 AGATGTTAA 129
RESULT 14
US-09-428-805-9
Sequence 9, Application US/09428805
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for

TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 77210
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/428,805
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/766,355
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT:063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 327 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: one-of(244, 305)
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "N = A or C or G or T"
US-09-428-805-9
Query Match 85.4%; Score 117.8; DB 4; Length 327;
Best Local Similarity 94.6%; Pred. No. 6.6e-35;
Matches 122; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 10 GAGAAATTGGCAGATTAATATAGGGGACCATGCTTTAGTGGTGTGACACTGACACTGACA 69
DB 1 GAGAAATTGGCGATAGTATAGGGGACCATGCTTTAGTGGTGTGACACTGACACTGACA 60
QY 70 ACCAAAGAGAACGAGTAGTGAAGGTGAGGAGCAGCTCCGCTGCTGGTACTTAA 129
DB 61 ACCAAAGAGAACGAGTAGTGAAGGTGAGGAGCAGCTCCGCTGCTGGTACTTAA 120
QY 130 AGATGTTAA 138
DB 121 AGATGTTAA 129
RESULT 15
US-08-766-355-6
Sequence 6, Application US/08766355
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee

Thu May 8 10:51:00 2003

us-10-010-731-13_copy_105_242.rni

Page 8

STREET : P.O. Box 77210
CITY : Houston
STATE : Texas
COUNTRY : United States of America
ZIP : 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER : IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,355
FILING DATE: Concurrently herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Ritchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT-063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEO ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified base
LOCATION: one-of(17, 265)
OTHER INFORMATION: /mod_base=OTHER
OTHER INFORMATION: /note= "N" - A or C or G or T
US-08-766-355-6

Query Match	62.8%	Score 86.6	DB 3	Length 293
Best Local Similarity	83.1%	Pred. No. 3.1e23		
Matches 98	Conservative 0	Mismatches 20	Indels 0	Gaps 0
QY	4	ACATGTGAGATTGGCGCAGATTAATATATAGGGGACCATGCTTAGTGTTGATGACTAC	63	
DB	176	ACTGTGTGAAATTGGCTTACACATACACAGGGGACCATGCTTGGTGTGTACTTTCAC	235	
QY	64	TGCACAAACCAAGAGACGACGATTGTGTGAAGGTATAGGAGACGACTCCGCTGCTGT	121	
DB	236	TGCACAAACCAAGACACTTACTTAGCCGAGAGGTACAGGAGACGACTCCGCTGCTGCT	293	

Search completed: May 8, 2003, 07:20:53
Job time : 17.2611 secs

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2003, 05:48:03 ; Search time 45.4873 Seconds
(Without alignments)
3770.133 Million cell updates/sec

Title: US-10-010-731-13_COPY_105_242

Perfect score: 138

Sequence: 1 AGAACAATGAGAAATTTGGC.....GGTGTACTAAAGATGTAA 138

Scoring table: IDENTITY_NNC

Gapop 10.0, Gapext 1.0

Searched: 783854 seqs, 621352466 residues

Total number of hits satisfying chosen parameters: 1567708

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PC7_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	138	100.0	250	9	US-10-010-731-13
2	138	100.0	490	9	US-10-010-731-19
3	138	100.0	507	9	US-10-010-731-10
4	120.8	87.5	189	9	US-10-010-731-18
5	119.4	86.5	200	9	US-10-010-731-5
6	117.8	85.4	327	9	US-10-010-731-9
7	86.6	62.8	293	9	US-10-010-731-6
8	64.8	47.0	420	9	US-10-178-213-436
9	64.4	46.7	563	9	US-10-178-213-439
10	61.4	44.5	494	9	US-09-805-694B-5
11	57.6	41.7	461	9	US-10-178-213-451
12	43.6	31.6	464	9	US-10-178-213-379
13	40	29.3	141	10	US-09-759-584-35
14	39	28.3	47	9	US-10-010-731-12
15	30.2	21.9	463	9	US-09-918-995-11517
16	30	21.7	2172	10	US-09-822-830A-440
17	29	21.0	1937	10	US-09-822-830A-364
18	28.8	20.9	15109	7	US-08-781-986A-44
19	28.6	20.7	1544	10	US-09-726-774-10

20	28	20.3	1503841	9	US-09-946-807-1	Sequence 1, Appli
21	28	20.3	1503841	10	US-09-795-668-1	Sequence 1, Appli
22	28	20.3	1503841	10	US-09-795-668-1	Sequence 1, Appli
23	27.6	20.0	32249	9	US-09-764-891-7364	Sequence 7364, Ap
24	27.4	19.9	1815	9	US-10-107-649-1	Sequence 1, Appli
25	27.4	19.9	1936	10	US-09-822-830A-291	Sequence 291, Ap
26	26.8	19.4	449	9	US-09-535-459-1813	Sequence 1813, Ap
27	26.8	19.4	449	9	US-10-092-154-328	Sequence 328, App
28	26.8	19.4	449	10	US-09-764-847-328	Sequence 328, App
29	26.8	19.4	31871	9	US-10-092-154-1403	Sequence 1403, Ap
30	26.8	19.4	31871	10	US-09-764-847-1403	Sequence 1403, Ap
31	26.4	19.1	393	9	US-09-796-692-8003	Sequence 8003, Ap
32	26.4	19.1	393	9	US-10-040-662-8003	Sequence 8003, Ap
33	26.4	19.1	1419	9	US-10-108-605-140	Sequence 140, App
34	26.2	19.0	190	10	US-09-880-107-132	Sequence 132, App
35	26.2	19.0	293	9	US-10-060-036-2476	Sequence 2476, Ap
36	26.2	19.0	561	10	US-09-962-436-115	Sequence 115, App
37	26.2	19.0	1639	9	US-09-764-868-99	Sequence 99, Appl
38	26.2	19.0	1661	9	US-09-764-868-512	Sequence 512, App
39	26.2	19.0	1661	9	US-09-764-891-2554	Sequence 2554, Ap
40	26.2	19.0	17200	10	US-09-764-877-3390	Sequence 3390, Ap
41	26.2	19.0	106344	9	US-09-910-185-10	Sequence 10, Appl
42	26	18.8	426	9	US-09-736-457-913	Sequence 913, App
43	26	18.8	426	9	US-09-902-541-913	Sequence 913, App
44	26	18.8	426	9	US-09-849-626-913	Sequence 913, App
45	26	18.8	426	9	US-10-017-754-913	Sequence 913, App

ALIGNMENTS

RESULT 1
US-10-010-731-13
Sequence 13, Application US/10010731
Publication No. US20030041347A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip Maganlal
Wu, Yonnie S.
Rosenberger, Cindy A.
Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,731
FILING DATE: 13-NO. US20030041347A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/003,198
FILING DATE: 07-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Paterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT.193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-010-731-13

Query Match 100.0%; Score 138; DB 9; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4e-38;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGCATGTGAGAAATTTGGCAGATTAATATAGGGGACCATGCTTTGTGTGTGACACT 60
|||||
DB 105 AGAAGCATGTGAGAAATTTGGCAGATTAATATAGGGGACCATGCTTTGTGTGTGACACT 164
|||||
QY 61 CACTGCACACCAAGAGAACGAGTGTAGTGAAGGAGTAGGAGACGACTTCGCTGCTGG 120
|||||
DB 165 CACTGCACACCAAGAGAACGAGTGTAGTGAAGGAGTAGGAGACGACTTCGCTGCTGG 224
|||||
QY 121 TGTACTAAAAAGATGTTAA 138
|||||
DB 225 TGTACTAAAAAGATGTTAA 242

RESULT 2
US-10-010-731-19
; Sequence 19, Application US/10010731
; Publication No. US20030041347A1
GENERAL INFORMATION:

APPLICANT: Liang, Jihong

Shah, Dilip Maganlal

Wu, Yonnie S.

Rosenberger, Cindy A.

Hakimi, Salim

TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/010,731

FILING DATE: 13-No. US20030041347A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/003,198

FILING DATE: 07-JAN-1998

ATTORNEY/AGENT INFORMATION:

NAME: Patterson, Melinda L.

REGISTRATION NUMBER: 33,062

REFERENCE/DOCKET NUMBER: MOBT:193

TELECOMMUNICATION INFORMATION:

TELEPHONE: (713) 787-1400

TELEFAX: (713) 787-1440

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 490 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-010-731-19

Query Match 100.0%; Score 138; DB 9; Length 490;
Best Local Similarity 100.0%; Pred. No. 1.9e-38;

Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGCATGTGAGAAATTTGGCAGATTAATATAGGGGACCATGCTTTGTGTGTGACACT 60
|||||
DB 156 AGAAGCATGTGAGAAATTTGGCAGATTAATATAGGGGACCATGCTTTGTGTGTGACACT 215
|||||
QY 61 CACTGCACACCAAGAGAACGAGTGTAGTGAAGGAGTAGGAGACGACTTCGCTGCTGG 120
|||||
DB 216 CACTGCACACCAAGAGAACGAGTGTAGTGAAGGAGTAGGAGACGACTTCGCTGCTGG 275
|||||
QY 121 TGTACTAAAAAGATGTTAA 138
|||||
DB 276 TGTACTAAAAAGATGTTAA 293

RESULT 3
US-10-010-731-10
; Sequence 10, Application US/10010731
; Publication No. US20030041347A1
GENERAL INFORMATION:

APPLICANT: Liang, Jihong

Shah, Dilip Maganlal

Wu, Yonnie S.

Rosenberger, Cindy A.

Hakimi, Salim

TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/010,731

FILING DATE: 13-No. US20030041347A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/003,198

FILING DATE: 07-JAN-1998

ATTORNEY/AGENT INFORMATION:

NAME: Patterson, Melinda L.

REGISTRATION NUMBER: 33,062

REFERENCE/DOCKET NUMBER: MOBT:193

TELECOMMUNICATION INFORMATION:

TELEPHONE: (713) 787-1400

TELEFAX: (713) 787-1440

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 507 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

FEATURE:

NAME/KEY: modified_base

LOCATION: one-of(17, 424, 485)

OTHER INFORMATION: /mod_base= OTHER

/note= "N" = A or C or G or T"

SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-010-731-10

Query Match 100.0%; Score 138; DB 9; Length 507;
Best Local Similarity 100.0%; Pred. No. 1.9e-38;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGCATGTGAGAAATTTGGCAGATTAATATAGGGGACCATGCTTTGTGTGTGACACT 60

Db 173 AGAACAATGTGAGATTGGCGAGATAAATATAGGGGACCATCTTTAGGTGTGACACT 232
|||
QY 61 CACTGCACAAACCAAGAACGCGAGTTAGTGAAGGTGTAGGACGACTTCGGTGTGG 120
|||||
Db 233 CACTGCACAAACCAAGAACGCGAGTTAGTGAAGGTGTAGGACGACTTCGGTGTGG 292
|||||
QY 121 TGTACTAAAGATGTAA 138
|||||
Db 293 TGTACTAAAGATGTAA 310
|||||

RESULT 4

US-10-010-731-18
; Sequence 18, Application US/10010731
; Publication No. US20030041347A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; Shah, Dilip Maganlal
; Wu, Yonnie S.
; Rosenberger, Cindy A.
; Haximi, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/010, 731
; FILING DATE: 13-NO. US20030041347A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/003, 198
; FILING DATE: 07-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Paterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 787-1400
; TELEFAX: (713) 787-1440
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 189 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-010-731-18

Query Match 87.5%; Score 120.8; DB 9; Length 189;
Best Local Similarity 98.4%; Pred. No. 1.3e-32;
Matches 122; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AGAACAATGTGAGATTGGCGAGATAAATATAGGGGACCATCTTTAGGTGTGACACT 60
|||||
Db 63 AGAACAATGTGAGATTGGCGAGATAAATATAGGGGACCATCTTTAGGTGTGACACT 122
|||||
QY 61 CACTGCACAAACCAAGAACGCGAGTTAGTGAAGGTGTAGGACGACTTCGGTGTGG 120
|||||
Db 123 CACTGCACAAACCAAGAACGCGAGTTAGTGAAGGTGTAGGACGACTTCGGTGTGG 182
|||||
QY 121 TGTAA 124

Db 183 TGGA 186
|||

RESULT 5

US-10-010-731-5
; Sequence 5, Application US/10010731
; Publication No. US20030041347A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; Shah, Dilip Maganlal
; Wu, Yonnie S.
; Rosenberger, Cindy A.
; Haximi, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/010, 731
; FILING DATE: 13-NO. US20030041347A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/003, 198
; FILING DATE: 07-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Paterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 787-1400
; TELEFAX: (713) 787-1440
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 17
; OTHER INFORMATION: /mod_base= OTHER
; /note= "N = A or G or T"
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-010-731-5

Query Match 86.5%; Score 119.4; DB 9; Length 200;
Best Local Similarity 99.2%; Pred. No. 4.2e-32;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AGAACAATGTGAGATTGGCGAGATAAATATAGGGGACCATCTTTAGGTGTGACACT 60
|||||
Db 80 AGAACAATGTGAGATTGGCGAGATAAATATAGGGGACCATCTTTAGGTGTGACACT 139
|||||
QY 61 CACTGCACAAACCAAGAACGCGAGTTAGTGAAGGTGTAGGACGACTTCGGTGTGG 120
|||||
Db 140 CACTGCACAAACCAAGAACGCGAGTTAGTGAAGGTGTAGGACGACTTCGGTGTGG 199
|||||
QY 121 T 121
|
Db 200 T 200

```
RESULT 6
US-10-010-731-9
; Sequence 9, Application US/10010731
; Publication No. US20030041347A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
;              Shah, Dilip Maganlal
;              Wu, Yonnie S.
;              Rosenberger, Cindy A.
;              Hakimi, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
;                   Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/010,731
; FILING DATE: 13-NO. US20030041347A1-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 09/003,198
; FILING DATE: 07-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 787-1400
; TELEFAX: (713) 787-1440
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 327 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified base
; LOCATION: one-of(244,305)
; OTHER INFORMATION: /mod_base= OTHER
; /note= "N" = A or C or G or T"
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-010-731-9

Query Match      85.4%; Score 117.8; DB 9; Length 327;
Best Local Similarity 94.6%; Pred. No. 1.8e-31;
Matches 122; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 10 GAGAAATTTGGCAATATATATAGGAGCAGCTTGTAGTGTGACACTGACAC 69
DB 1 GAGAAATTTGGCGATTAAGATTAAGGAGCAGCTTGTAGTGTGACACTGACAC 60
QY 70 ACCAAGAGAGACGCACTTAGTGAAGGTGTAGGAGCAGCTTCCGCTGTGTACTAA 129
DB 61 ACCAAGAGAGACGCACTTAGTGAAGGTGTAGGAGCAGCTTCCGCTGTGTACTAA 120
QY 130 AGATGTAA 138
DB 121 AGATGTAA 129

RESULT 7
US-10-010-731-6
```

```
; Sequence 6, Application US/10010731
; Publication No. US20030041347A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
;              Shah, Dilip Maganlal
;              Wu, Yonnie S.
;              Rosenberger, Cindy A.
;              Hakimi, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
;                   Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/010,731
; FILING DATE: 13-NO. US20030041347A1-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 09/003,198
; FILING DATE: 07-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 787-1400
; TELEFAX: (713) 787-1440
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified base
; LOCATION: one-of(17,265)
; OTHER INFORMATION: /mod_base= OTHER
; /note= "N" = A or C or G or T"
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-010-731-6

Query Match      62.8%; Score 86.6; DB 9; Length 293;
Best Local Similarity 83.1%; Pred. No. 1.4e-20;
Matches 98; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 4 ACATGTGAGAAATTTGGCAGATTAATATAGGAGCAGCTTGTAGTGTGACACTAC 63
DB 176 ACTTGTGAGAAATTTGGCTTAACATTAACAGGAGCAGCTTGTGTGACTTTAC 235
QY 64 TGCACACCAAGAGAGACGCACTTAGTGAAGGTGTAGGAGCAGCTTCCGCTGTGT 121
DB 236 TGCACACCAAGAGAGACGCACTTAGTGAAGGTGTAGGAGCAGCTTCCGCTGTGT 293

RESULT 8
US-10-178-213-436
; Sequence 436, Application US/10178213
; Publication No. US20030041348A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvey, Leslie
; APPLICANT: Cahoon, Rebecca
```



```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,584
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/377,687
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-759-584-35

Query Match          29.0%; Score 40; DB 10; Length 141;
Best Local Similarity 60.6%; Pred. No. 0.00021;
Matches 83; Conservative 0; Mismatches 48; Indels 6; Gaps 1;

QY 4 ACATGTGAGAAATTTGGCAGATAAATATAGGGACATGCTTTAGTGT-----TGTGAC 57
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 4 ACTGGAGAACCTTCTTGAACCTTCAAGGACCATGCTCCAGATGGAACATCGAAC 63

QY 58 ACCTACTGCACCAACCAAGAACGCGATTAGTGAAGGTGTGGGACGCTCCGCTGC 117
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 64 AACCATTTGGAAGAACGACGATCTTCTTCTGGAAGATGACAGATGATTCNNNTGC 123

QY 118 TGGTGTACTAAAGATG 134
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 124 TGGTGCACCTAGAAACTG 140

RESULT 14
US-10-010-731-12/c
; Sequence 12, Application US/10010731
; Publication No. US20030041347A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip Maganlal
Wu, Yonnie S.
Rosenberger, Cindy A.
Hakim, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,731
FILING DATE: 13-NO. US20030041347A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/003,198
FILING DATE: 07-JAN-1998
ATTORNEY/AGENT INFORMATION:

```

```

NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-010-731-12

Query Match          28.3%; Score 39; DB 9; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 AGGAGAGACTCCGCTGCTGTACTATAAAGATGTTAA 138
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 47 AGGAGAGACTCCGCTGCTGTACTATAAAGATGTTAA 9

RESULT 15
US-09-918-995-11517/c
; Sequence 11517, Application US/09918995
; Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/918,995
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 11517
LENGTH: 463
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(463)
OTHER INFORMATION: n = A,T,C or G
US-09-918-995-11517

Query Match          21.9%; Score 30.2; DB 9; Length 463;
Best Local Similarity 58.2%; Pred. No. 0.91;
Matches 53; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 3 AACATGTGAGAAATTTGGCAGATAAATATAGGGACATGCTTTAGTGTGACACTCA 62
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 434 AACATGGGGGAACCTTCAAGCATTAATTTTGGCAATATATTTTGGATATGACACCA 375

QY 63 CTGCACACCAAGAGACGCACTTACTGGA 93
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 374 AAGCACACGACACAGAACGCAATAATATGA 344

Search completed: May 8, 2003, 07:21:33
Job time : 47.4873 secs

```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2003, 05:40:33 ; Search time 500.799 Seconds

(without alignments)
4462.820 Million cell updates/sec

Title: US-10-010-731-13_COPY_105_242

Perfect score: 138
Sequence: 1 AGACATGAGAGATTGGC.....GGCTACTAAAGATGTAA 138

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: em_estda:*
2: em_esthm:*
3: em_estln:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_hiv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	111	80.4	446	9	AJ498901 AJ498901
2	58.6	42.5	426	12	BG838678 BG838678
3	58.2	42.2	487	13	BI321179 BI321179
4	58	42.0	517	9	AJ308155 AJ308155
5	49	35.5	366	13	BI321308 BI321308
6	43.6	31.6	574	14	BQ151477 BQ151477

7	40.8	29.6	503	12	BF633403 BF633403
8	38.6	28.0	438	13	BI642738 BI642738
9	35.2	25.5	686	17	AG181132 AG181132
10	32.6	23.6	1637	12	BG247486 BG247486
11	31.8	23.0	542	17	AO793341 AO793341
12	31.8	22.5	433	17	AZ512910 AZ512910
13	30.8	22.3	567	10	BE330295 BE330295
14	30.8	22.3	662	10	BB356735 BB356735
15	30.6	22.2	149	17	AZ395343 AZ395343
16	30.6	22.2	437	14	BQ119258 BQ119258
17	30.4	22.0	788	14	BE560644 BE560644
18	30	21.7	464	17	AZ013758 AZ013758
19	30	21.7	1055	12	BE888496 BE888496
20	29.8	21.6	997	17	CNS062626 CNS062626
21	29.6	21.4	281	10	BB287165 BB287165
22	29.6	21.4	294	10	BB173276 BB173276
23	29.6	21.4	299	10	BB265616 BB265616
24	29.6	21.4	335	17	AZ021720 AZ021720
25	29.6	21.4	342	17	AZ004823 AZ004823
26	29.6	21.4	805	10	BE469462 BE469462
27	29.6	21.4	1007	17	CNS06M20 CNS06M20
28	29.4	21.3	250	9	AV113248 AV113248
29	29.4	21.3	290	10	BB369954 BB369954
30	29.4	21.3	522	12	BF419465 BF419465
31	29.4	21.3	540	14	BQ985543 BQ985543
32	29.4	21.3	540	14	BQ994036 BQ994036
33	29.4	21.3	582	17	AZ968358 AZ968358
34	29.4	21.3	655	17	BH120322 BH120322
35	29.4	21.3	813	17	AQ364702 AQ364702
36	29.4	21.3	331	10	BB731530 BB731530
37	29.2	21.2	412	10	BB835814 BB835814
38	29.2	21.2	418	10	BB833130 BB833130
39	29.2	21.2	453	10	BB820106 BB820106
40	29.2	21.2	453	10	BB820106 BB820106
41	29	21.0	398	9	AA582705 AA582705
42	29	21.0	660	9	AU237466 AU237466
43	29	21.0	660	13	BI101794 BI101794
44	29	21.0	676	12	BG546289 BG546289
45	28.8	20.9	327	9	AV090308 AV090308

ALIGNMENTS

RESULT 1
AJ498901
LOCUS 446 bp mRNA linear EST 09-AUG-2002
DEFINITION AJ498901 MPOSE Medicago truncatula cDNA clone mt--acc955209h10,
mRNA sequence.
ACCESSION AJ498901
VERSION AJ498901.1 GI:22089344
KEYWORDS
SOURCE
ORGANISM
barrel medic.
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
1 (bases 1 to 446)
Firnhaber,C., Bartelsmeier,V., Meyer,F., Bartels,D., Bekel,T.,
Linke,B., Puhler,A. and Kuester,H.
Determination of transcript sequences from developing pods
Including seeds of Medicago truncatula genotype A17
Unpublished (2002)
Contact: Kuester H
Lehrstuhl fuer Genetik
Universitaet Bielefeld
Postfach 100131, D-33501 Bielefeld, Germany.
Location/Qualifiers
1..446
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="mt--acc955209h10"

```

/clone_11b-"MPPOSE"
/tissue_type="pods including seeds"
/dev_stage="different stages of development"
/notes="Vector: pGEM-T; Site.1: PstI; Site.2: SphI;
genotype A17; cDNA was prepared from polyA+ enriched RNA
from developing pods including seeds harvested at
different stages of development. The cDNA was
directionally ligated by Medigenomix into the pGEM-T
vector from Promega using GCATCGCGCGGCGCGCATG and
CTCGAGCGCATTAATGCGCGG adapters. Plasmids containing cDNA
inserts were propagated in E. coli DH10B cells."
BASE COUNT      147 a      84 c      83 g      132 t
ORIGIN
Query Match      80.4%; Score 111; DB 9; Length 446;
Best Local Similarity 88.9%; Pred. No. 1.5e-26;
Matches 120; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 4 ACATGTGAGAAATTTGGCAGATAAATATATAGGAGCAGCTGCTTATGTTGATGACACTGAC 63
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 145 ACTTGGAGAAATTTGGCTGATTAATACAGGAGCAGCATCTTATGTTGATGATCTAC 204
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 64 TGCACACCAAGAGAGAGCAGTGTAGTGTAGGAGCAGCTCCGCTCGCTGCT 123
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 205 TGCACCTACCAAGAGAGAGTGTAGGAGCAGTGTAGGAGCAGCTTCTGTTGTTGCT 264
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 124 ACTAAAGATGTTAA 138
    ||| ||| ||| |||
DB 265 ACTAAAGATGTTAA 279
    ||| ||| ||| |||

RESULT 2
BG838678      426 bp      mRNA      linear      EST 25-MAY-2001
LOCUS      GC01_03f01_A GC01_AAFRC_ECORC_cold_stressed_Glycine_clandestina
DEFINITION      Glycine clandestina cDNA clone GC01_03f01, mRNA sequence.
ACCESSION      BG838678
VERSION      BG838678.1 GI:14204985
KEYWORDS      EST.
SOURCE      Glycine clandestina.
ORGANISM      Glycine clandestina.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE      1 (bases 1 to 426)
AUTHORS      Singh, J.A., Farah, S., Chapados, J., Couroux, P., De Moors, A., Harris,
              L.J., Hattori, J.I., Ouellet, T., Robert, L.S., Sprott, D. and Tinker,
              N.A.
TITLE      Expressed Sequence Tags from Cold-Stressed Glycine clandestina
              Seedlings
JOURNAL      Unpublished (2001)
COMMENT      Contact: Singh, J.A.
              Eastern Cereal and Oilseed Research Centre
              Agriculture and Agri-Food Canada
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
              Tel: (613) 759-1662
              Fax: (613) 759-1701
              Email: singhja@agr.ca.
              Location/Qualifiers
FEATURES
source      1..426
              /organism="Glycine clandestina"
              /cultivar="1035"
              /db_xref="taxon:45687"
              /clone="GC01_03f01"
              /clone_11b="GC01_AAFRC_ECORC_cold_stressed_Glycine_clandest
              ina"
              /tissue_type="leaves, stem"
              /note="Vector: Bluescript SK+/XhoI-EcoRI; Site.1: EcoRI;
              Site.2: XhoI; Plants incubated at 2 degrees under 12 hours
              of light/day. Harvested after only 2-3 days of cold
              treatment. cDNA was prepared with the Uni-Zap cDNA kit

```

```

from Stratagene. Eco RI adapters were linked followed by
digest with Xho I/Eco RI and ligated to pBluescript."
BASE COUNT      116 a      92 c      86 g      125 t
ORIGIN
Query Match      42.5%; Score 58.6; DB 12; Length 426;
Best Local Similarity 67.4%; Pred. No. 5.5e-09;
Matches 95; Conservative 4; Mismatches 36; Indels 6; Gaps 1;

QY 4 ACATGTGAGAAATTTGGCAGATAAATATATAGGAGCAGCTGCTTA-----GTGGTTGTGAC 57
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 316 ACTTGGAGAAATTTGGCTGATTAATACAGGAGCAGCATCTTATGTTGATGATCTGCT 257
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 58 ACTCACTGCACACCAAGAGAGCAGCTTGTAGGAGCAGCAGCTCCGCTGC 117
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 256 GATCACTGCACACCAAGAGAGCAGCTTGTAGGAGCAGCAGCAGCAATTTGCTGCH 197
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 118 TGTGTACTAAAGATGTTAA 138
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 196 TGHGCGACAGCAAACTGTTAA 176
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 3
BI321179      487 bp      mRNA      linear      EST 29-NOV-2001
LOCUS      sat48d10.y3 Gm-cl077 glycine max cDNA clone GENOME SYSTEMS CLONE
DEFINITION      ID: Gm-cl077-1723 5', similar to SW:10KD_VIGUN P18646 10 KD PROTEIN
              PRECURSOR ;, mRNA sequence.
ACCESSION      BI321179
VERSION      BI321179.1 GI:15000365
KEYWORDS      EST.
SOURCE      soybean.
ORGANISM      Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE      1 (bases 1 to 487)
AUTHORS      Shoemaker, R., Kelm, P., Vodkin, L., Erpelting, J., Corvelli, V., Khanna,
              A., Bolla, B., Merritt, M., Hillier, L., Kuehn, T., Martin, J., Beck, C.,
              Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers,
              T., Pearson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk,
              R., Ritter, E., Kohn, S., Shih, T., Jackson, Y., Cardenas, M., McCann,
              R., Waterston, R. and Wilson, R.
TITLE      Public Soybean EST Project
JOURNAL      Unpublished (1999)
COMMENT      Contact: Shoemaker R/Public Soybean EST Project
              Public Soybean EST Project
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: est@watson.wustl.edu
              Putative full length read
              vector to vector length is This clone is available through: Reegen,
              Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801
              For further information call: (800)-533-4363 or contact via email:
              coueresgen.com
              Seq primer: -40RP from gibco
              High quality sequence stop: 432.
              Location/Qualifiers
FEATURES
source      1..487
              /organism="Glycine max"
              /db_xref="taxon:3847"
              /clone="GENOME SYSTEMS CLONE ID: Gm-cl077-1723"
              /clone_11b="Gm-cl077"
              /tissue_type="18 day old 'Williams' seedlings"
              /dev_stage="18 day old 'Williams' seedlings"
              /lab_host="DH10B"
              /note="Vector: pBluescript II SK+; Site.1: EcoRI; Site.2:
              XhoI; The mRNA was isolated from cotyledons of 18-day-old
              'Williams' seedlings which were greenhouse grown in
              potting soil. The cotyledons were flash-frozen in liquid

```


potting soil. The coryledons were flash-frozen in liquid nitrogen. StrataGene's cDNA Synthesis Kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of StrataGene's first-strand synthesis primer was used. An 'anchor' nucleotide (V-A, C, or G) was added to the 3' end of the primer [GACAGACAGACAGACAGACAGACACTGCTCGAG(T)18V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA, ligated to EcoRI adaptors and subsequently phosphorylated. The cDNA was then precipitated and redissolved in sterile, RNase-, DNase-free water. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI from Promega (400U/ul); all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using Sephacryl S-500 High Resolution (Pharmacia Biotech) in a 2-mm diameter column and a bed volume of approximately 1ml. The column eluent was precipitated, redissolved, and ligated into StrataGene's pBluescript II XR predigested vector (pBluescript II SK(+)) vector that has been digested with EcoRI and XhoI, and phosphorylated by StrataGene. This library was constructed in the laboratory of Dr. Paul Kelm and Dr. Virginia H. Coryell at Northern Arizona University."

[illegible]

FEATURES	source
location/Qualifiers	1. .574
/organism="Medicago truncatula"	
/db_xref="taxon:3880"	
/clone="NF088A06LE"	
/clone_1lb="Developing leaf"	
/tissue_type="leaf"	
/dev_stage="Pooled developmental"	
/note="Vector: lambda zap. Contains a mixture of very young, developing, mature and senescing leaves."	
BASE COUNT	198 a 104 c 104 g 167 t 1 others
ORIGIN	

Query Match	31.6%	Score 43.6	DB 14	Length 574
Best Local Similarity	66.7%	Pred. No. 0.00068		
Matches 96	Conservative 0	Mismatches 39	Indels 9	Gaps 2
QY 1	AGACATGTGAGATTTTGGCATGATTAATATATAGGGACCATCTTTA-----GTGGTTG	54		
Db 140	AGACATTGTGAGCATTTTGGCTGATCATACAGAGACCATCTTTCAAGGAAGTACTGT	199		
QY 55	GACCTCACTGCACCAACCAAGAGACGCACTTAGTGGAAAGTGTATAGGACGACTTCGC	114		
Db 200	GATGACCACTGCACCAACCAAGACACACTTAATATATAGTGGACAGTCC---ATACTTTCAA	256		
QY 115	TGCTGTGTACTTAAAGATCTTAA	138		
Db 257	TGTTTCTGCATCAAAACGTTAA	280		

	RESULT 7			
	Bf633403			
LOCUS	NF047E03Drf1E1022 Drought Medicago truncatula CDNA clone NF047E03Df 5', mRNA sequence.	503 bp	mRNA	EST 19-DEC-2000
DEFINITION	Bf633403			
ACCESSION	Bf633403.1 GI:11897561			
VERSION	EST.			
KEYWORDS	bartel medtc. Medicago truncatula Euariyola; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots: Rosidae; eurosids I; Fabales; Fabbaceae; Papilionoideae; Trifoliaee;			
SOURCE	Medicago.			
ORGANISM	1 (bases 1 to 503) Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula drought library Unpublished (2000)			
JOURNAL COMMENT	Contact: May GD Plant Biology Division The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7391 Fax: 580 221 7380 Email: gdmay@noble.org			
	Insert Length: 503 Std Error: 0.00 Plate: 047 row: E column: 03 Seq primer: TCACCAGCAAACTGATGC.			
FEATURES	location/Qualifiers			
source	1..503 /organism="Medicago truncatula" /db_xref="taxon:3880" /cclone="NF047E03DT" /cloned_lib="Drought" /tissue_type="Planklets" /dev_stage="Pooled timepoints" /note="Vector: lambda Zap; Contains a mixture of entire planklets harvested in a series of days-post-watering timepoints."			
BASE COUNT	181 a 82 c 93 g 147 t			
BRIGIN				

Query Match 29.6%; Score 40.8; DB 12; Length 503;
Best Local Similarity 65.3%; Pred. No. 0.0056;
Matches 94; Conservative 0; Mismatches 42; Indels 8; Gaps 2;

OY 1 AGAATGTGAGAAATTTGGCAGATTAATATAGGGACATGCTTAA-----GTGGTGT 54
DB 146 AGGACTTGTGAGCATTTGATGATACATACAGAGCAGCATGCTTCACGAGAGTAGCTGT 205
OY 55 GACATCTGACTGACACCAACCAAGAACGAGTGTAGAGGTGTAGGACACTTCCGC 114
DB 206 GATGACCACTGCGAACCAACACACACTTAATAGTGACCGT--GCCATTAACCTTCA 263
OY 115 TGCTGTGACTAAAGATGTAA 138
DB 264 TGTTCCTGACCTCAAAACTGTAA 287

RESULT 8 438 bp mRNA linear EST 10-SEP-2001
BI642738
LOCUS T2S1161 T2S (Sapwood-heartwood transition zone of black locust -
DEFINITION Summer) Robinia pseudoacacia cDNA, mRNA sequence.
ACCESSION BI642738
VERSION BI642738.1 GI:15544948
KEYWORDS EST.
SOURCE Robinia pseudoacacia.
ORGANISM Robinia pseudoacacia.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Robinieae;
Robinia.
1 (bases 1 to 438)
REFERENCE Han, K.-H., Yang, J., Park, S., Paule, C.R., Kapur, V., Retzel, E.F.,
Kandem, D.P. and Keathley, D.E.
TITLE Analysis of gene expression patterns in trunk wood of a mature
black locust (Robinia pseudoacacia)
JOURNAL Unpublished (2002)
COMMENT Contact: Kyung-Whan Han
Department of Forestry
Michigan State University
126 Natural Resources, East Lansing, MI 48824-1222, USA
Tel: 517 353 4751
Fax: 517 432 1143
Email: hank@emsu.edu.

FEATURES
Source location/Qualifiers
1..438
/organism="Robinia pseudoacacia"
/db_xref="taxon:35938"
/clone_lib="T2S (Sapwood-heartwood transition zone of
black locust - Summer)"
/tissue_type="sapwood-heartwood transition zone"
/dev_stage="mature tree"
/note="Vector: lambda Triplex; Site_1: Sfi I; Site_2: Sfi
I; The cDNA library was made from the sapwood-heartwood
transition zone of a mature black locust tree collected in
Michigan in late July."

BASE COUNT 134 a 80 c 86 g 124 t 14 others
ORIGIN

Query Match 28.0%; Score 38.6; DB 13; Length 438;
Best Local Similarity 63.1%; Pred. No. 0.029;
Matches 89; Conservative 0; Mismatches 45; Indels 7; Gaps 2;

OY 4 ACATGTGAGATTTGGCAGATTAATATAGGACCATG-----CTTAGTGTGTGTAC 57
DB 126 ACTTGTGAGAACCTGGCTGACATTCAGGGGTCTATGATCACCCTGCTACTCGCGAC 185
OY 58 ACTCACTGACACCAACCAAGAACGAGTGTAGAGGTGTAGGAGGACACTTCGCGAC 117
DB 186 GATCACTGCAAGNTCNNNNA-CACCTTACTCACTGCGCAGGTGCGAGACGATTTGGCTNG 244
OY 118 TGGTGTACTAAAGATGTAA 138

DB 245 GGGTGACCAAAACTGTAA 265

RESULT 9 686 bp DNA linear GSS 09-JAN-2002
AG181132/C
LOCUS Pan troglodytes DNA, clone: RP43-053017.TJ, genomic survey
DEFINITION sequence.
ACCESSION AG181132
VERSION AG181132.1 GI:16710812
KEYWORDS GSS.
SOURCE Pan troglodytes male lymphocytes DNA, clone: RP43-053017.TJ.
ORGANISM Male BAC library clone: RP43-053017.TJ.
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

REFERENCE Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE BAC end sequences of library RPCI-43
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 686)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan
1-7-22 Suhei-cho, Tsukuba, Ibaraki, Japan, Tokyo, Kanagawa 230-0045, Japan
(E-mail: chimpbes@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
end was generated during the Red process and may have higher chance
of clone cracking errors.
PRIMERS
Sequencing: TJ
LIBRARY
Vector : pBAC3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI
Location/Qualifiers
1..686
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-053017.TJ"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC library"

BASE COUNT 179 a 147 c 160 g 200 t
ORIGIN

Query Match 25.5%; Score 35.2; DB 17; Length 686;
Best Local Similarity 55.8%; Pred. No. 0.48;
Matches 67; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

OY 8 GTGAGATTTGGCAGATTAATATAGGACCATGCTTATGAGGTGTGACACTGCA 67
DB 531 GGGTAATTAAGCTGAGACCTATTTGGCTGCACTTCTCAGAGAGTTATGCAATTCRAAGC 472
OY 68 CAACCAAGAGAACGAGTGTAGGAGGACGACACTTCGCTGCTGTACTA 127
DB 471 ACAGATTAATAACAGAGGTTGGTGTATAGGTCACAAAGACCTTCTGATATATA 412

RESULT 10 1637 bp mRNA linear EST 13-FEB-2001
BG247486
LOCUS BG247486/C
DEFINITION 62360241P1 NCI_CGAP Mam1 Mus musculus cDNA clone IMAGE:4488491 5',
mRNA sequence.
ACCESSION BG247486
VERSION BG247486.1 GI:12757301
KEYWORDS EST.
SOURCE house mouse.

High quality sequence stop: 433.

FEATURES
Location/Qualifiers

1..433
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U061M0358117"
/clone_1bp="Mouse 10kb plasmid U061M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42uv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114[9D]AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 109 a 105 c 81 g 138 t

ORIGIN

Query Match 22.5%; Score 31; DB 17; Length 433;

Best Local Similarity 51.9%; Pred. No. 10;

Matches 70; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 4 ACATGTGAGATTGGCAGATTAATATAGGGACCATCTTATGTTGTGACACTGAC 63

Db 293 AAAGTCAACCTTACATAGAGAGTTAAGCAGCTTGAATCCTGACACCTGTC 234

QY 64 TGCACAAACCAAGAACGAGTTCGAAAGGTGAGGAGCAGCTTCGCTGCTGT 123

Db 233 TGAATAAAAAAGAGGGGGGTGTAGAGTGTAGAGACTTACCTTACTAGTAAC 174

QY 124 ACTAAAGATGTAA 138

Db 173 GCTTAAGTGTAA 159

RESULT 13

BE330295

LOCUS

DEFINITION 567 bp mRNA linear EST 04-DEC-2001

ACCESSION BE330295

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

Public Soybean EST Project
Unpublished (1999)

COMMENT

Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 1479 Std Error: 0.00
High quality sequence stop: 468.

FEATURES
source

1..567

/organism="Glycine max"

/db_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-c1040-1522"

/clone_1bp="Gm-c1040"

/tissue_type="Hypocotyl and Plumule, germinating seeds"

/lab_host="DH10B"

/note="Vector: pT73Pac (Pharmacia); Site_1: EcoRI;

Site_2: NotI; This cDNA library was constructed from mRNA

isolated from hypocotyl and plumule tissues of seeds

germinated for three days of the cultivar Williams 82.

Complementary DNA was synthesized from mRNA using a primer

consisting of a poly(dT) sequence with a NotI restriction

site. EcoRI adaptors were ligated to the blunt-ended cDNA

fragments followed by digestions with EcoRI and NotI. The

cDNA fragments were directionally cloned into the

EcoRI-NotI restriction site of the pT73-Pac vector. The

ligated cDNA fragments were transformed into DH10B host

cells (Gibco BRL). This library was constructed by Dr.

Randy Shoemaker."

BASE COUNT 153 a 106 c 138 g 168 t

ORIGIN

Query Match 22.3%; Score 30.8; DB 10; Length 567;

Best Local Similarity 58.9%; Pred. No. 13;

Matches 53; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 6 ATGTGAGATTGGCAGATTAATATAGGGACCATCTTATGTTGTGACACTGACTG 65

Db 350 ATGCCAAAGCAGAGATTAATATGAAATATACATCATTAAGATTCCCAATATATG 409

QY 66 CACAACCAAGAGAACGAGTTCGAAAG 95

Db 410 GACTTGAAGAAAGAAACCAAGCTCATGGAAG 439

RESULT 14

BB356735/C

LOCUS

DEFINITION 662 bp mRNA linear EST 24-OCT-2001

ACCESSION BB356735

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

Public Soybean EST Project
Unpublished (2001)
On Jul 12, 2000 this sequence version replaced g1:9068563.
Contact: Yoshinide Hayashizaki

Query Match 22.2%; Score 30.6; DB 17; Length 149;
 Best Local Similarity 68.9%; Pred. No. 8.9;
 Matches 42; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 OY 40 TGCCTTAGTGGTGTGACACTGACACACCAAGAGACCGAGTTAGTGAAGTGT 99
 Db 21 TCCTTACAGTTGTGTGACATGCTGCTAAAGCAATGAGAAAGAAATGGAAGTGC 80
 OY 100 A 100
 Db 81 A 81

Search completed: May 8, 2003, 07:15:49
 Job time : 505.799 secs

THIS PAGE BLANK (00)